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   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SEQUENCE
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER
                                                         DOMAIN
TRANSMEM
                                                                                            PROSITE;
                                                                                                                                                         EMBL;
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-96111955; PubMed-8777713;

Wiley S.R., Schooley K., Smolak P.J.,

Nicholl J.K., Sutherland G.R., Davis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TN10_MOUSE
                                                                                                                                                                                                                                                                                                                                              "Identification and characterization family that induces apoptosis."; Immunity 3:673-682(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APOPTOSIS INDUCING LIGAND) TNFSF10 OR TRAIL.
                                             DOMAIN
                                                                               Cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                               SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN
TISSUE SPECIFICITY: WIDESPREAD.
                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                     FUNCTION: INDUCES APOPTOSIS
                                                                                                                                              ; U37522; AA(
MGI:107414;
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                                                                                                                       PF00229;
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; PS50049; TNF_2;
e; Transmembrane;
e; Transmembrane;
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M 18 38
39 291
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281
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_1; 1.
_2; 1.
_1ne; Signal-anchor; Apoptosis.
17 CYTOPLASMIC (POTENTIAL).
38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
391 EXTRACELLULAR (POTENTIAL).
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Pred. No. 1.1
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EXTRACELLULAR (POTENTIAL).
DDAAAF78DAAB2F6D CRC64;
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Davis-Smith T.,
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Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 134
                                                                                                                                                                                                                                                                                                                                                                                                                               TNIL MOUSE STANDARU;

TNIL MOUSE STANDARU;

O35235; O35306;

O1-OCT-2000 (Rel. 40, Created)

O1-OCT-2000 (Rel. 40, Last sequence update)

O1-OCT-2000 (Rel. 40, Last annotation update)

TUMOR NECROSIS FACTOR LIGAND SUPERPAMILY MEMBER 11 (RECEPTOR ACTIVATOR OF NUCLEAR FACTOR KAPPA B LIGAND) (RANKL) (TWP-RELATED ACTIVATION-INDUCED CYTOKINE) (TRANCE) (OSTEOPROTEGERIN LIGAND) (OPGL) (OSTEOCLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM TISSUE-97460112; PubMed=9312132; MEDLINE=97460112; PubMed=9312132; Robinson E., Bartlett F.S. I.
                                                                                                                                                       MEDLINE=98227661; PubMed=9568710;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J.,
Burgess T., Elliott R., Colombero A., Elliott
Sullivan J., Hawkins N., Davy E., Capparelli C
Kaufman S., Sarosi I., Shalhoub V., Senaldi G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
          Yasuda H., Shima N., Nakagawa N., Yamaguchi K.,
Mochizuki S.-I., Tomoyasu A., Yano K., Goto M.,
Morinaga T., Higashio K., Udagawa N., Takahashi
"Osteoclast differentiation factor is a ligand
                                                                                                        "Osteoprotegerin ligand is differentiation and activat Cell 93:165-176(1998).
                                                                                                                                                                                                     MEDLINE-98227661; P
                                                         TISSUE=Bone marrow stroma;
MEDLINE=98188248; PubMed=9520411;
                                                                                                                                                                                                                                                                     that
                                                                                                                                                                                                                                                                                             Choi
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                               Boyle W.J.;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                  "TRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
                                                                                                                                                                                                                                                                    activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMDHEASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRIFVSVTNEHLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-----IKENTKNDKQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRTFQDTISTVPEKQLSTPPLPRGGRPQKVAAHITGTTRRSNSALIPISKDGKTLGQKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLDQEASFFGAFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
134; Conser
                                                                                                                                                                                                                                                       is a novel ligand of the tumor tivates c-Jun N-terminal kinase . Chem. 272:25190-25194(1997).
                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
                                                                                                                      gand is a cytokine activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
33477
                                                                                                                                                                                                                                                                                                                                                                                           Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.6%;
69.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (F
3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                      Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      693;
No. 1.
                                                                                                                                  that regulates
                                                                                                                                                                                                                                                                    necrosis factor receptor family
in T cells.";
                                                                                                                                                                                                                                                                                                      ., Orlinick
                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
.3e-52;
                                                                                                                                                            G.,
                                                                                                                                                                                                                                                                                                                                                                                          Muridae;
                                                                                                                                                                      c.,
                                                                                                                                                                                                                                                                                                        Frankel
., Kinosaki
., Murakami
hi N., Suda
d for
factor and
                                                                                                                                                                    Dunstan C.R.,
G., Scully S., Hsu H.,
C., Eli A., Qian Y.-X.,
                                                                                                                                                          Guo J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                       J.,
el w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                   osteoclast
                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
                                                                                                                                                                                                                                                                                                      Chao
.N., I
                                                                                                                                                          Delaney
                        H > X
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                                                                                                                                                                                                                                                                                                        Lee
                                                                                                                                                                                                                                                                                                                    .
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                                    Tsuda
                                                                                                                                                                                                                                                                                                                                                                                           Mus
                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                            ٦.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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Query Match
Best Local S
Matches 65
                                                                                                             CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF053713; AAC40113.1; -. EMBL; AF013170; AAC71061.1; -. EMBL; AB008426; BAA25425.1; -. EMBL; AF019048; AAB86812.1; -. EMBL; AB036798; BAA97259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Thymic lymphoma;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Do
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F.,
                                                                                                                                                                                                                                                                                                                                                       EMBL; AB036798; BamGD; MGI:1100089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                          Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                              CARBOHYD
                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                          InterPro; IPR003263; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl.
                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000478; -.
                                                                                                                                                                                                                                             ignal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANCE/RANKL.";
 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN TELLS.
BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
TRABECULAR BONE AND LUNG.
DISEASE: DEFICIENCY IN THESF11 RESULTS IN FAILURE TO FORM LOBULO-
ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH
NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
HYPERTROPHIC CHONDROCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homologue of the TNF receptor and its ligand enhance T-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES
NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR. AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 SEETI --
                                                Similarity
                                                                                                                                                                                                                                                                           PS00251; TNF_1; FALSE_NEG PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                          Differentiation;
                                                                                                         99
316
                                                                                                                                             70
197
262
                                 Conservative
                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                             TNF;
                                                                                                               A,
                                                                                                      316
197
262
99
34944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sci. U.S.A. 95:3597-3602(1998)
                                                                                                                                                                                                             48
69
                                                23.6%;
-STVQEKQQNISPLVRERGPQRVA-
                                                                                                                Œ,
                                                                                                                                                                                                                                                            Receptor; Glycoprotein; Transmembrane;
                               37;
                          Pred. No. 3e-17; Mismatches
                                                                                                                          (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL)
G -> D (IN REF. 4).
                                                Score 235.5;
Pred. No. 3e
                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE II
                                                                                                             -> D (IN REF. 4).
08DF63A2BE00967A CRC64;
                                                3e-13;
                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dougall W.C.,
                                                                                                                                                                                                             II MEMBRANE PROTEIN)
                                                            Length
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       уд
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                 316;
                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN THE
                               Gaps
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CRETTAR REPRESENTATION OF COLUMN AND COLUMN 
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TN11_H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cancer cells responsible for encoding a secreted form of formation.";
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Thymocytes; MEDLINE=97460112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Osteoprotegerin ligand is a cytokine differentiation and activation."; Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu Sullivan J., Hawkins N., Davy E., Capparelli C., Ell A., Qian Y.-Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lymph node; MEDLINE-98227661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A homologue of the TNF receptor and and dendritic-cell function."; Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Bone marrow, and Peripheral blood;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dometsko M.E., Roux E.R., Teepe M.C., DuBose R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFSF11 OR RANKL OR TRANCE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF NUCLEAR FACTOR KAPPA B LIGAND) (RANKL) (TNF-RELA: INDUCED CYTOKINE) (TRANCE) (OSTEOPROTEGERIN LIGAND) DIFFERENTIATION FACTOR) (ODF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                               MEDLINE=20175237;
                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 73-317 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boyle W.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                           TISSUE=Tongue;
                                                                                                                                                                                                                                                                            that
                                                                                                                                                                                                                                                                                                   TRANCE is a novel ligand of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 FYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                  Biol.
  FUNCTION:
                                                                                                                                                                                                                                                                            activates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 89
                          Biophys.
                                                                                                                                                                                                                                                  Chem.
                                                                                                                                                                                                                                                                                                                                               Rho J., Arron J., Robinson E
S., Cayani E., Bartlett F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 node;
                                                                                                                                                                                                N.A. (ISOFORM
OSTEOCLAST DIFFERENTIATION AND
                                                                                                                                                                                                                                            c-Jun N-terminal kinas
272:25190-25194(1997).
                                                                                                                                                 PubMed=10708588;
                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9312132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9568710;
                          Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·INAASIPSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQD
                                                                                                                                                                                                                                                                         N-terminal kinase
                            Commun.
                                                                                                  Sato N.;
le for humoral
                                                                        ODF/TRANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPGL
                          269:532-536(2000)
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                                                                        hypercalcemia
E that induces
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                                                                                                                                                                                                                                                                                                   necrosis factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulates osteoclast
                                                                                                                                                                                                                                                                            cells.";
ACTIVATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312
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                                                                                                  express mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                           osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delaney J.,
                                                                                                                                                                                                                                                                                                                                                  S.Y.,
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RESULT 5
FASL_MOUSE
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Best Local S
Matches 52
       FASL_MOUSE STANDARD; PRT; 2
P41047; Q61217; Q9R1F2;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up)
01-OCT-2000 (Rel. 40, Last annotation)
FAS ANTIGEN LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000478; -. InterPro; IPR003263; -. Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                              276
                                                                                                                                                                                            153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BL; AF019047; AAB86811.1; -.
3L; AF053712; AAC39731.1; -.
3L; AF013171; AAC51762.1; -.
3L; AB037599; BAA30488.1; -.
4; 602642; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROTD. INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECRETED (ISOFORM 2).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SOF PRODUCED BY ALTERNATIVE SPLICING.
PRODUCED BY ALTERNATIVE HIGHEST IN THE PERIPHERAL LYMPH NODES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS BETWEEN T CELLS AND DENDRITIC CELLS RAW PLAY & ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL HYPERCALCEMIA OF MALIGNANCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
                                                                                                                                                             NVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                         YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
                                                                                                                                                                                                                        LYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSI
                                                                                                                                                                                                                                                                                                          AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 93
                                                                                                                                                                                                                                                    IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 152
                                                                                                                                                                                                                                                                                AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYY
ဝ္က
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00251; TNF_1; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                 194
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
171
198
                                                                                                                                                                                                                                                                                                                                             Conservative
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OR FASL OR
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171
198
73
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35478
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                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
GLD
                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (P
MISSING (IN ISOFORM 2).
A -> G (IN REF. 3).
; 766176446348097F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
N-LINKED (GLCNAC. . .) (F
N-LINKED (GLCNAC. . .) (F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                         232.5;
No. 5.4
                                        update)
                                                                                     279
                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
DR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                       DB
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                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                         317;
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HEART,
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                 215
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MEDLINE-96091792; PubMed-7495745;
Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
Rahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
Rousseau M., Bron C., Renno T., French L., Tschopp J.;
"Characterization of the non-functional Fas ligand of gld mice.";
"Characterization of the non-functional Fas ligand of gld mice.";
Int. Immunol. 7:1381-1386(1995).

11. TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED II
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C3H; TISSUE=Spleen;
MEDLINE=20021694; PubMed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: A new alter
spliced product of the mouse Fas ligand gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lynch D.H., Watson M.L., Alderson M.R., Baum Tough T., Gibson M., Davis-Smith T., Smith C. "The mouse Fas-ligand gene is mutated in gld
                                                  between
                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION OF VARIANT GLD MEDLINE=96091792; PubMed=749574!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNF family gene cluster.";
Immunity 1:131-136(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM FASL).
MEDLINE=95196085; PubMed=7889405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generalized lymphoproliferative mutation in the Fas ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM FASL). MEDLINE=94185175; PubMed=7511063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   two amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95388076; PubMed=7544870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 76:969-976(1994).
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mus musculus Balb/c
two amino acids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fenner M.H., Shioda T., Isselbacher K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peitsch M.J., Tschopp J.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative molecular modelling of the TNF family.";
                                                                                                                                                                                                 INTERACTION.
DISEASE: A DEFICIENCY IN THIS
                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: ISOFORM F
                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT. FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN STIMULATED SUICIDE OF MATURE AND ADDRESS OF THE ANTIGEN SUICIDE OF THE SUICIDE OF THE SUICIDE OF THE SUI
                                                                                                                            SIMILARITY: BELONGS
                                                                                                                                                 DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
                                                                                                                                                                                                                                                                                                                                ISOFORM FASLS IS SOLUBLE.
                                                                                                                                                                                                                                                                                                                                                                                                          T CELLS, OR BOTH
                                                                       SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunol. 32:761-772(1995).
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                                          the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fas ligand
                                                                                                                            TO THE TUMOR NECROSIS FACTOR FAMILY
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Mammalia; Eutheria;
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Glycoprotein; Signal-anchor; Apoptosis;
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T -> A (IN STRAIN BALB/C).
E -> G (IN STRAIN BALB/C).
F -> L (IN GLD; ABOLISHES
TO ITS RECEPTOR).
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Pred. No. 2.8e-09;
6; Mismatches 59;
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BY SIMILARITY
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Catarrhini;
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ED (GLCNAC...) (POTE)
ED (GLCNAC...) (POTE)
G (IN ISOFORM FASLS).
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                                                                                                          Vertebrata; Euteleostomi;
                                                                                           Hominidae;
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                                                                                               Pfam; PF00229; TNF; 1.
PROSITE; PS00251; TNF_1;
PROSITE; PS50049; TNF_2;
                                                                                                                                                         EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                           "Human Fas ligand: gene structure, specificity."; Int. Immunol. 6:1567-1574(1994).
                                                                                                                                                                                                                                                                                       This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Schaetzlein C.E.,
                                                                                                                                       HSSP; P01375;
MIM; 134638; -
                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Role of Fas ligand in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95071350; Put
Mita E., Hayashi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schaetzlein
                                                                    TRANSMEM
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MEDLINE=95127560; PubMed=7826947;
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lymphocytes
                                                                               DOMAIN
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                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                     T CELLS, OR BOTH.
SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II M
                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                 x89102; CAA61474.1;

U08137; AAC50071.1;

U11821; AAC5124.1;

U11822; BAA07320.1;

D38122; BAA07320.1;

CAB09424.1;
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                                                                                                                                                 2TUN.
                                                                                                                                                          BAA32542.1;
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195) to the
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                                                                                                                                                                                                                                                          institutions as long as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis
                                    1.
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1.
Glycoprotein; Signal-anchor; Apoptosis.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                              TYPE II MEMBRANE
R FLUID, PROBABLY
                                                                                                                                                                                                                                                                                                                                                                    IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R., Philippsen P.,
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
POLY-PRO.
BY SIMILARITY.
N-LINKED (GLCN
N-LINKED (GLCN
N-LINKED (GLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takehara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204:468-474(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.,
                                                                                                                                                                                                                                                                                                                                                                    ANTIGEN-STIMULATED SUICIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., Abe T., Suda T., Nagata S.;
chromosomal location and species
) (GLCNAC.
) (GLCNAC.
                                                                                                                                                                                                                                     (See http://www.isb-sib.
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BY CLEAVAGE I
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OF MATURE
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SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
 PROSITE;
                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94084792; PubMed-7505205;
Suda T., Takahashi T., Golstein P., Nagata S.;
"Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.";
Cell 75:1169-1178(1993).
-I- FUNCTION: CYPORKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FASS ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PASIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                           InterPro; IPR000478; -
Pfam; PF00229; TNF; 1.
                                                                                    the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P36940;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
FAS ANTIGEN LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNPSF6 OR APTILG1 OR FASL.
                                                          EMBL; U03470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FASL_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
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                                                                                                                                                                                                                                                                               T CELLS, OR BOTH.

T CELLS, OR BOTH.

SUBUNIT: HOMOTRIMER (PROBABLE).

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY

SUBCELLULAR FLUID, PROBABLY BY CLEAVAGE F
                                                                                                                                                                                                             SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                         THYMOCYTES. MODERATE KIDNEY AND LUNG.
                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY:
                                                                                                                                                                                                                           INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLVNFEESQTFFGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYMRNSKYPQDLVMMEGKMMSYCTTGQMWAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IY-KYTSYPDPILLMKSARNS------CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LEWEDT-YGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                          AAC52129.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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TNF_1;
TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31485
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27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279
                                                                                                                                                                                                                                                                      EXPRESSED IN ACTIVATED
                                                                                                                                                                                                                                                        OR WEAK EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                             THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A8A6EB358246E9BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SSYLGAVFNLTSADHLYVNVSE 263
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                                                                                                                                                                                                                                                        FOUND
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                                                                                                                                                                                                                                                                       SPLENOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 281
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                                                                                                                                                                                                                                                        SMALL
                                                                                                                                                                                                                                                                                                                 BE RELEASED
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                                                                                                                                                                                                                                                        INTESTINES
                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                  collaboration
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TN14_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 50
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DISULFID
CARBOHYD
CARBOHYD
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     TN14_HUMAN STANDARD; PRT; 240 AA.
043557; 075476;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine;
DOMAIN
                                                   growth.";
J. Biol. Chem.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98122340; PubMed=9462508;
MCDLINE=98122340; PubMed=9462508;
MOREOTE R., MOREOTE P., KO
                                                                                                                  Tan K.B., Dede K., Spampanato J., Silverman DiPrinzio R., Emery J.G., Deen K., Eichman (
                                                                                                                                                                                                               "LIGHT, a new member of ligands for herpesvirus Immunity 8:21-30(1998).
                                                                                                                                                                                                                                                                                                                                                                                  MEDIATOR-LIGAND) (HVEM-L).
TNFSF14 OR LIGHT OR HVEML.
                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR LIGAND MEDIATOR-LIGAND) (HVEM-L).
                                        ÷
                                                                               HVEM/TR2,
                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                         Truneh A.,
                                                                                                                                                        MEDLINE=98438532; PubMed=9765287;
                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                        ware
                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                            Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D.,
                                                                            Herpesvirus entry mediator ligand Herpesvirus entry mediator ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 LY 276
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FUNCTION: ACTIVATES NEKB, STIMULATES THE PROLIFERATION OF T CELLS, AND INHIBITS GROWTH OF THE ADENOCARCINOMA HT-29. ENGAGES THE RECEPTOR FOR THE LYMPHOTOXIN-ALPHA-BETA HETEROTEXHER BUT DOES NOT FORM COMPLEXES WITH EITHER LT-ALPHA OR LT-BETA. ACTS AS A RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISTVQEKQQNISPLVRERGPQRVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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100 278
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230
116
116
247
257
278 AA; 31140 M
                                                                                                       Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                     273:27548-27556(1998)
                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                                                      AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%;
27.5%;
                                                                                                                                                                                                                           entry mediator.
                                                                                                                                                                                                                                         the TNF superfamily, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POT M-LINKED (GLCNAC. . .) (POT M-) 2898E18A862CEAC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN). EXTRACELLULAR (POTENTIAL). PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oprotein; Signal-anchor; Apoptosis CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177.5; DB 1
No. 2.5e-08;
                                                                             (HVEM-L), a novel ligand of T cells and inhibits F
                                                                                                                                                                                                                                                                              Kochel K.D., Cheung
                                                                                                                                                                                                                                                                 R.J.,
                                                                                                                                                                                                                                                                                                                                               Hominidae;
                                                                                                                   C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                 c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCNSQPLSHKVYMRNFKYP
                                                                                                                     Chabot-Fletcher M.,
                                                                                                                                                                                                                                                                   Cohen
                                                                                                                                                                                                                                                                                                                                                                                                            14 (HERPESVIRUS
                                                                                                                                  Hensley
                                                                                                                                                                                                                                         lymphotoxin alpha are
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                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                 G.H.,
                                                                                                                                    P.
                                                                                                                                               Minton
                                                                                HT29
                                                                                                                                                                                                                                                                   Spear P.G.,
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 A RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                               ENTRY
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RESULT
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Best Local S
Matches 50
                                                                                                                                      01-OCT-1996
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30-MAY-2000
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CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                BOVIN
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Bovidae; Bovinae;
NCBI_TaxID=9913;
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                     TNFSF5 OR CD40LG
                                                                                                                      CD40 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF036581;
                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Cytotoxin;
                                                                                                                                                                                                            rnf5_bovin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000478;
                                                                                                                                                                                                                                                                                                 231
                                                                                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNTT: HOMOTRIMER:
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
                                                                                                                                                                                                                                                                                                 TRSYFGAFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR NONHEMATOPOIETIC TUMOR LINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOR HERPES SIMPLEX VIRUS
                                                                                                                                                                                                                                                                                                                                  EASFFGAFLV 190
                                                                                                                                                                                                                                                                                                                                                                                     -SYPDPILLMKSARNSCWSKDAEYGLY--SIYQGGIFELKENDRIFVSVTNEHLIDM-DH
                                                                                                                                                                                                                                                                                                                                                                                                                                        DGALVVTKAGYYYIYSK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQY----
                                                                                                                                                                                                                                                                                                                                                                 PRYPEELELLVSQQSPCGRATSSSRVWWDSSFLGGVVHLEAGEEVVVRVLDERLVRLRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIQERRSHEVNPAAHLTGANSSLTGSGGP------LLWE-TQLGLAFLRGLSYH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF064090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00251; TNF_1; FALSE_NEG. PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102
214
240
                                                                   (Bovine).
                                                                                                                      (Rel. 34, Created)
(Rel. 34, Last sequence
(Rel. 39, Last annotation
(TNF-RELATED ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC39563.1; -.
AAC25169.1; -.
                                                                                                                                                                                                                                                                                                 240
                                                                                     OR CD40L.
                  Bos.
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102
214
26351
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58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Signal-anchor.
37 CYTOPLASMIC (POTENTIAL).
58 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                        annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 152; DB 1;
Pred. No. 3.2e-06;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL)

E -> K (IN REF. 2).
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49D0BF67E1390B39
                                                                                                                 on update)
PROTEIN) (TRAP) (T CELL ANTIGEN
                                                                                                                                                       update)
                                                                                                                                                                                                            261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                Euteleostomi;
cora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IYKYT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collaboration
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RESULT 10
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                 13-AUG-1987 (Rel. C
13-AUG-1987 (Rel. C
15-JUL-1999 (Rel. 3
TUMOR NECROSIS FACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                     TNFA_RABIT P04924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A MEDLINE=91065534;
                                     NCBI_TaxID=9986;
                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                        TNF OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z48469; CAA88363.1; HSSP; P29965; 1ALY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenetics 42:430-431(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96006582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                         130
                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                 147
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                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor necrosis factor alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF C STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4. INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                RILLRAANTHSSSKPC--GQQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFG
                                                                                                                                                                                                                                                                                                                                                          VQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 72
                                                                                                                                                                                                                                                        ILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                                 VKKKEKNEEMHKGDQEPQ-IAAHV-----ISEASSKTTSVL-----QW--APKGYY 146
                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;; PS00251; TNF_1;
;; PS50049; TNF_2;
;e; Transmembrane;
1 22
M 23 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000478; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              47
178
240
261
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                    FACTOR
                                                                                                                                                                 STANDARD;
                                                                                                                38,
05,
05,
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Muriuki M., Gai
 PubMed=2249779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
218
240
29242
                                                 Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; 1.
2; 1.
2; 1.
ie; Glycoprotein; Signal-anchor.
2 CYTOPLASMIC (POTENTIAL).
2 SIGNAL-ANCHOR (TYPE-II ME)
6 'POTENTIAL). 'POTENTIAL)
                                                                                                Last sequence update)
Last annotation update)
PRECURSOR (TNF-ALPHA) (CACHECTIN)
                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                              Score 142; DB
Pred. No. 2.6e-
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
N-LINKED (GLCNAC. . .) (F
8491FEFB30A787FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaidulis
                                                                                                                                                                 PRT;
                                                  Leporidae;
                                                                                                                                                                 235
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                                                                                                                                                                                                                                                                                                                                                                                              6e-05;
                                                  Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 261;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN)
                                                                                                                                                                                                                                257
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STITITE OF REAL PROPERTY OF THE PROPERTY OF TH
Query Match
Best Local S
Matches 42
                                                                                                                                                                                                         InterPro; IPR000478; -.
InterPro; IPR002959; -.
InterPro; IPR002959; -.
InterPro; IPR002959; -.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISECT.
PRINTS; PR01235; TNF 1; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS0049; TNF_2; 1.
Outokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                           DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
Hayashi H., Kato M., Seko M.;
"Molecular cloning and expression in Escherichia coli of the cDNA
coding for rabbit tumor necrosis factor.";
DNA 5:149-156(1986).
-i- PUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKIN
MITH A WIDE VARIETY OF FUNCTIONS: IT ICAN CAUSE CYTOLYSIS OF
CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding TNF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor.";
DNA 5:157-165(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wallace R.B.;
"Molecular cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86219712; PubMed-3519138; Ito H., Shirai T., Yamamoto S., Akira M.,
                                                                                                                                                                                FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86219711; PubMed=3519137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        BL; M12845; AAA31486.1; -.
BL; M12846; AAA31482.1; -.
BL; M60340; AAA31484.1; -.
R; A25451; A25451.
R; A25454; A25454.
R; JS0727; JS0727; JS0727;
SP; P01375; ITNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMOTRIMER.
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE
SUBCELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANCER AND INFECTION, AND AND MALNUTRITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISEASE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEOLYTIC PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONDITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
    Similarity 23.
42; Conservative
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                                                                                                         148
63
235
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                                                                                              79
235
56
179
63
25816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (lymphotoxin)
                    13.7%;
23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
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                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE TUMOR NECROSIS FACTOR FAMILY.
    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Azizov M.M., Jongeneel C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rabbit TNF locus,
                                                                                                                                  SIGNAL-ANCHOR (TYPE-II
BY SIMILARITY.
MISSING (IN REF. 3).
                  Score 136.5;
Pred. No. 6.
                                                                                                                                                                                                  TUMOR NECROSIS FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SI
                                                                                                           ISSING (IN REF. 3).
610177D0BD2EF871 CRC64;
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    Mismatches
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5.7e-05;
hes 81;
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                                         DB 1;
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    Indels
                                           Length
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                                             235;
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    23;
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01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
01-NOV-1997 (Rel. 3
 CARBOHYD
SEQUENCE
                                   Cytokine;
SIGNAL
                                                           PROSITE;
                                                                                                                                 PIR; S17289; S17289.
InterPro; IPR000478; -.
                                                                                                                                                                                                                                                                                         -!- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED
IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS
-!- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND
OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SU
-!- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                   "The porcine tumor necrosis factor-encoding comparative analysis.";
Gene 102:171-178(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIG
                                                                                  PRINTS; PR01234; TNECROSISFCT PRINTS; PR01236; TNFBETA.
                                                                                                                                                                                            modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                     use
                         CHAIN
                                                                                                                                                          EMBL;
                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91340150; PubMed=1874444;
Kuhnert P., Wuethrich C., Peterha
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTA OR TNFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYMPHOTOXIN-ALPHA
                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFB_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
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                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLANGMKLTDNQLVVPADGLYLIYSQVLFSGQ
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                                                                                                          PF00229; TNF; 1
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                                                                                                                                                          X54859; CAA38638.1;
                                                         PS50049; TNF_1; 1.
                                                                                                                                                                                                                    non-profit institutions as long
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                                               Glycoprotein;
                                                                                                                       IPR002960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
 95
204 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23, Created)
23, Last sequence update)
35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRECURSOR
 95
21960 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
                                               Cytotoxin;
                                                                                                                                                                                                                                                                                                                                                                                        Peterhans E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LT-ALPHA) (TNF-BETA).
LYMPHOTOXIN-ALPHA.
N-LINKED (GLCNAC.
; 81263187435E56AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
                                                                                                                                                                                             noved. Usage by and fc
(See http://www.isb-sib.
                                                                                                                                                                                                                                  There are no
                                                                                                                                                                                                                                                                                                                                                                                        Pauli U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                     RODUCED BY LYMPHOCYTES WE CELLS IN VITRO AND IN ETA AND ONE ALPHA SUBUNITS.
                                                                                                                                                                                                                     as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GCRSYVLLTHTVSRFAVSYPNK
                                                                                                                                                                                                                                                                                                                                                                            genes: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suidae;
..) (POTENTIAL)
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                restrictions on
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                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                              collaboration
L outstation -
                                                                                                                                                                                              .ch/announce/
                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                      in
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                                                                                                                                                                                                                     no
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Query Match
Best Local Similarity
Matches 46; Conser

Conservative

13.5%;

Score 134.5; Pred. No. 8.

Mismatches

3.3e-05; 76;

Length

204;

33;

Gaps

7;

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RESULT 12
TNFA_CAVPO
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                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT 1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-DUNKIN-HARTLEY;
MEDLINE-97462215; PubMed-9316485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P51435;
01-OCT-1996
             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yuan H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-HARTLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         factor-alpha.
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                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE
PROTEOLYTIC PROCESSING (BY SIMILARITY).
DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEA
CANCER AND INFECTION, AND IS CHARACTERIZED BY GI
                                                                                                                                                                                                                                                            SUBUNIT: HOMOTRIMER (B
SUBCELLULAR LOCATION:
EXTRACELLULAR SOLUBLE
PTM: THE SOLUBLE FORM
                                                                                                                                                                                                                                                                                                                                                FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKIN MITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                       SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                       CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR TNFA
                                                                                                                                                                                                                                                                                                                      CONDITIONS
                                                                                                                                                                                                          AND
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                          U39839;
U77036;
                                                                                                                                                                                                                                                                                                                                                                                                                          Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .M., Yoshimura T., Smith A.W., Westwiinflammation induced by recombinant
                                                                                                                                                                                                       MALNUTRITION.
                                                                                                                                                                                                                                                                                                                                      PROLIFERATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                          HOMOTRIMER (BY SIMILARITY).
                          AAB06492.1;
AAB19210.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Lung;
y F.J., Bingl
                                                                                                                                                                                                                                                                                                                                                                                                                          273:L524-L530(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bingle C.D.;
o the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                    INDUCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Eute
Hystricognathi; Caviidae;
                                                                                                                                                                                       TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                    CELL DIFFERENTIATION UNDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Westwick J.,
binant guinea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CACHECTIN)
                                                                                                                                                                                       FACTOR FAMILY
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                                                                                                                                                                                                                    DISEASES,
BY GENERAL
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                                                                                                                                                                                                                                                               FORM
                                                                                                                                                                                                                                                                                           ALSO
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                                                                                                                                               collaboration
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TNFA_PIG
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Best Local
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PROSITE; PS50049; TNF_2; 1.

CYTOKINe; CYTOTOXIN; Transmembrane; G:
PROPEP 1 79 BY SIMILA

CHAIN 80 234 TUMOR NEC

TRANSMEM 36 56 SIGNAL-AI

DISULFID 147 178 BY SIMILA

SEQUENCE 234 AA; 25793 MW; 72727294
                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-91016861; PubMed=2216741;
Drews R.T., Coffee B.W., Prestwood A.K.,
"Gene sequence of porcine tumor necrosis
"Gene sequence of porcine tumor necrosis
"Sene sequence of sec
         SEQUENCE OF 44-232 FROM N.A. MEDILINE-90034181; PubMed=2478420; Pauli U., Beutler B., Peterhans E.; "Porcine tumor necrosis factor alpha: chain reaction and determination of the Gene 81:185-191(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFA_PIG P23563;
                                                                                                                                                                     "The porcine tumor necrosis comparative analysis."; Gene 102:171-178(1991).
                                                                                                                         TISSUE=Macrophage;
Choi C.S., Molitor T.W.,
                                                                                                                                                                                                       MEDLINE=91340150; Pubn
Kuhnert P., Wuethrich
                                                                                                                                                                                                                                                                                                                                                Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991
01-NOV-1991
                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01234; TNECROSISECT PRINTS; PR01235; TNFALPHA.
                                                                                          Anim.
                                                                                                    necrosis
                                                                                                                                                                                                                              FISSUE=Liver;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                               "Complete nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172
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                                                                                                                                                                                                                                                                                                                                                                                OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDPILLM 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAIKSPCQKETPEGAERKPWYEPIYLGGVFQLQKGDRLSAEVNLPQYLDFADSGQIYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSARNSCWSKDAEYG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPQREEQFSSGPPFRPLAQTLTLRSASQNDNDKPVAHVVANQQAEEELQWLSKRANALLA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPQRVAAHITGT---RGRSNTL---SSPNSKNEKALGRKINS------WESSRSGHSFL
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                                                                                          Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                       factor-alpha.";
otechnol. 2:97-105(1991).
                                                                                                                                                FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                   (Pig).
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                           FACTOR
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SI
                                                                                                                                                                                                                   PubMed=1874444;
                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
MAINLY
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24.6%;
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C
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PRECURSOR (TNF-ALPHA) (CACHECTIN).
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Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                           Lin
                                                                                                                                                                                                       Peterhans
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ω,
                                                                                                             of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embrane; Glycoprotein; SBY SIMILARITY.
TUMOR NECROSIS FACTOR
SIGNAL-ANCHOR (TYPE-II
BY SIMILARITY.
SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 132.5;
Pred. No. 0.00
33; Mismatches
                                                                                                                                                                                            factor-encoding
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the nucleo
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BY MACROPHAGES,
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                     loning with nucleotide
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nes 77;
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factor
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Р.
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                                                                                                                                                                                                                                                                        R.A.;
alpha.";
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                                                                                                               porcine
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                                the
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                                                                                                                                                                                                                                                                                                                                               Sus.
                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
ij
                               polymerase
SI
                                                                                                               tumor
A CYTOKINE
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RESULT L.
TNFA_PERLE
TNFA_PERLE
TNFA_939;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X54001; CAA37949.1; -.
EMBL; X54859; CAA38639.1; -.
EMBL; X57321; CAA40591.1; -.
EMBL; M29079; AAA31128.1; -.
PIR; S12606; S12606.
PIR; S17290; S17290.
PIR; S18965; S18965.
HSSP; P01375; ZTUN.
P36939;
01-JUN-1994 (Re
01-JUN-1994 (Re
15-JUL-1999 (Re
TUMOR NECROSIS
TNF OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1234; TNECROSISECT.
PRINTS; PRO1235; TNFALPHA.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS00251; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000478; -.
InterPro; IPR002959; -.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                               178
                                                                                                                                                                                                                                                      142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMOTRIMEN.
SUBCELLULAR LOCATION: TYPE
SUBCELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEAL!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR SOLUBLE FORM.
PTM: THE SOLUBLE FORM DERIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEOLYTIC PROCESSING.
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                                                                                                                                                                                                                                   SK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG
: :|: || ||:|:|:::||: :| :|
                                                                                                                                                                                                                                                                                          VVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQ
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                                                                                                                                                                                                               RETPEGAEAKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG
                                                                                                                                                                                                                                                                                                                                  VIHEKGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLMKSARNSCW 141
                                                                                                                                                                                                                                                                                                                                                                                                           GPORVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGEL
                                                                                                                                                                                                                                                                                                                                                                    GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Cytotoxin; Tro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36
144
232
                                    (Rel. 29,
(Rel. 29,
(Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                    STANDARD;
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56
176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.1%;
25.1%;
                                    Last sequence update)
Last annotation update)
                                                                            Created)
                      PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
; 65B28F702D99C8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 130;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR.
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                                                                                                                    PRT;
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                  (TNF-ALPHA) (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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ng as its content is in
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Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                           TRANSMEM
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     Cytokine; PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peromyscus leucopus (family Cricetidae).";

Immunogenetics 35:351-353(1937).

-i- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE

WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF

CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF

CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION

OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE

CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M59233; HSSP; P01375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crew M.D., Filipowsky M.E.;
"Sequence of the tumor necrosis factor/cachectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=92218012; PubMed=1348497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peromyscus.
NCBI_TaxID=10041;
                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01234; TNECROSISFCT. PRINTS; PR01235; TNFALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peromyscus leucopus (White-footed mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00229; TNF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                184
                                           169
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                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                    72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND MALNUTRITION.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONDITIONS.
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION:
EXTRACELLULAR SOLUBLE
-FFG
                                                                                                                                                                                            ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                        ALLANGMOLKONQLVIPADGLYLVYSQVLFKGQ
                                             VNLLSAIKSPC-PKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQ
                                                                          ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS
                                                                                                                                    SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 129
                                                                                                                                                                    IGPQREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGAN 113
                                                                                                                                                                                                                                                                                                                PRO1235; TNFALL.....

PSO0251; TNF_1; 1.

PSSO0251; TNF_2; 1.

PSSO049; TNE_2; 1.

PSSO049; Transmembrane; Glycoprotein; Signal-anchor.

BY SIMILARITY.

PSTONE PROTEIN).

PSTONE NECROSIS FACTOR.

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000478; -. IPR002959; -.
                186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
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235 l
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Pred. No. 0.00027;
9; Mismatches 75
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; 235A5CFC9F9AC624 CRC64;
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TNF5\_MOUSE

INF5\_MOUSE

STANDARD;

PRT;

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DISULFID
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Peaitsch M.C., Jongeneel C.V.;
Peaitsch M.C., Jongeneel C.V.;

"A 3-D model for the CD40 ligand predicts that it is a compact trimer similar to the tumor necrosis factors.";

Int. Immunol. 5:233-238(1993).
-1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.

INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
-1- SUBGULILLAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992
01-AUG-1992
30-MAY-2000
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"Emerging cytokine family.";
Nature 358:26-26(1992).
[3]
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MEDLINE-92244364; PubMed-1374165;
MEDLINE-92244364; PubMed-1374165;
Armitage R., Fanslow W., Sato T.A.,
Macduff B.M., Anderson D.M., Gimpel
Maliszewski C.R., Clark E.A., Smith
                                                                                                                                                        сив; ICDA; 31-OCT-93;
MGD; MGI:88337; Tnfe
                                                                                                                                                                                           EMBL; X65453; CAA46448.1;
PIR; S21738; S21738.
                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                     modified and this statement is not removed.
                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY TO THE THE FAMILY. MEDLINE=92310561; Pubmed=1377364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD40. "
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                                                                                       Cytokine;
                                                                                                                                                                                                                                                                                                                                                           - ! - SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 357:80-82(1992).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                 InterPro; IPR000478; -. Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                           FRANSMEM
                                                                           NIAMOC
                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular and biological characterization of a murine ligand for
                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR SOLUBLE FORM TISSUE SPECIFICITY: SPECIFI
                                                                               PS00251; TNF 1; 1.
PS50049; TNF_2; 1.
PS50049; TNF_2; 1.
Pransmembrane; Glycoprotein;
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 47
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(Rel. 23, Last sequence update)
(Rel. 39, Last annotation update)
(TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
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POTENTIAL.
N-LINKED (GLCNAC. .
                                                       oprotein; Signal-anchor; 3D-structure.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                             EXTRACELLULAR (POTENTIAL).
                                              (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clifford K.N., Strockbine L., S.D., Davis-Smith T., C.A., Grabstein K.H., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                        EXPRESSED
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VGLWLKPSIGSERILLKAANTHSSSQLCEQ--QSVHLGGVFELQAGASVFVNVT 241
                          QYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 171
                                                          ---QW-AKKGYYTMKSNLVMLENGKQLTVKREGLYYVYTQVTFCSNRE----PSSQRPFI
                                                                          KINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMV 117
                                                                                                                  RQFEDLVKDITLNKEEKKENSFEMQRGDEDPQIAAHV-----VSEANSNAASVL--
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15; Mismatches 68;
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Search completed: October 1, 2001, 11:44:41 Job time: 112 sec

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Minimum DB
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Copyright (c) 1993 - 2000 Comp
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US-08-996-139-13
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US-08-996-649-100-9
US-08-649-100-9
US-08-8110-453-2
US-08-8110-453-2
US-09-290-640-25
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US-08-883-086-10

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61,	Sequence 23, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	•	•	Sequence 6, Appli	Sequence 11, Appl	Sequence 2, Appli	Patent No. 5180811	Patent No. 5180811	Sequence 3, Appli	Sequence 2, Appli	Sequence 1, Appli

ALIGNMENTS

#### RESULT 1 US-08-670-354-2 Sequence 2, Application US/08670354 Patent No. 5763223 GENERAL INFORMATION: COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple 7.5.2 SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/670,354 FILING DATE: 25-JUN-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/496,632 FILING DATE: 29-JUN-1995 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin. TITLE OF INVENTION: Cytokine That Induces Apoptosis NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: CITY: Seattle STATE: WA ZIP: 98101 COUNTRY: ADDRESSEE: Katmy.... STREET: 51 University Street USA Kathryn A. Anderson, Floppy disk Immunex Corporation .0.1

; MOLECULE TYPE: US-08-670-354-2

TOPOLOGY:

linear

TELEFAX: (206) 233-064
TELEX: 756822
INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS

LENGTH: 281 amino acids
TYPE: amino acid

REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644

ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn
REGISTRATION NUMBER: 32,

гуп А. 32,172 sR: 2835-в CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0)
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435

US 08/548,368

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CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1
                                                                                                                   US-08-780-496-1

Sequence 1, Application US/08780496

; Patent No. 6046048

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-584-031-1
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Best Local Simi
Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08584031A Patent No. 6030945
                                               APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: A
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                              121 YKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH 180
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                 STREET:
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460 Point San Bruno Blvd
outh San Francisco
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                                   Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 3.8e-98;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08883086 Patent No. 6171787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE THE FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADBORESSE: ADBORESSE: ADBORESSE: 100 Abbott Park Road
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P097
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                                            ZIP:
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                             CITY: Abbott Park
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                                                                                                                                                              USA
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                                                                                   IBM Compatible
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ATTORNEY/AGENT INFORMATION:

FILING DATE:

APPLICATION NUMBER:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

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; MOLECULE TYPE: No. 6171787e
US-08-883-086-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9610895 GENERAL INFORMATION:
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REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
                                                                                                                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 29-JUN-1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 EASFFGAFLVG 191
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271 EASFFGAFLVG 281
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                 STREET: 51 Un:
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 INSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYI 120
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                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                 USA
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                                                                        29-JUN-1995
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                                                                                          US 08/496,632
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 Mismatches

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RESULT 6
US-09-105-343A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
OPERATING SYSTEM: Windo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT//
APPLICATION UNBER: PCT//
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 12-FEB-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MEMBER OF THE TITLE OF INVENTION: FOR TREATMENT NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 60 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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TELEX: 75682
                               NAME: BECKER, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Abbot
CITY: Abbott Park
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                                                                                                                                                                                                                            FastSEQ for Windows Version 2.0b
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                                                                                                              PCT/US98/02859
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Best Local :
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              TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
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SEQUENCE CHARACTERISTICS:
                                                             NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                              COMPOTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Vers
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
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TOPOLOGY: lin
MOLECULE TYPE:
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LENGTH: 177 amino acids
                                                                                                                                                                                                                         CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                        APPLICATION NUMBER: US 08/548,368 FILING DATE: 01-NOV-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/496,632 FILING DATE: 29-JUN-1995
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
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                                                (206) 233-0644
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; TOPOLOGY: 1;; MOLECULE TYPE: PCT-US96-10895-6
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Best Local Similarity
Matches 134; Conserv
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                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 291 amino acid
                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: MICROSOft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
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                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
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NUMBER OF SEQUENCES:
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                                                                                                           TELEFAX: (206
TELEX: 756822
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                              amino acid
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51 University Street
                                                              291 amino acids
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Cytokine That Induces Apoptosis
                                                                                                                              (206) 587-0430
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                                  linear
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             protein
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                                                                                                                                                                                                                                                                                  US 08/548,368
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 Best Loc
Matches
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Best Local 9
                                   Query Match
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048.US.P2
TELEFONMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFONMUNICATION:
TELEPHONE: 847-935-2623
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APPLICANT: WILEY, S.R.
                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows Version SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MEMBER OF THE TITLE OF INVENTION: FOR TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 DLDQEASFFGAFLI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 VQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 SWESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQL
 Local Similarity
nes 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                             TOPOLOGY:
                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/105,343A FILING DATE: 12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRIFVSVTNEHLM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-----IKENTKNDKQM 116
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                                                                                                                                                             amino acid
                                                                                                            TYPE:
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                                                                                                                                                                            183 amino acids
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abbott Laboratories
                                                                                                           No. 6207642e
                                                                                                                                            single
65.7%; Score 654; DB 4; 68.7%; Pred. No. 4.9e-62; ative 22; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.6%; Score 693; DB 5; I 69.1%; Pred. No. 6.8e-66; tive 23; Mismatches 31;
                                                                                                                                                                                                                                                                                                            6048.US.P2
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                                   Length 183;
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Gaps
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; MOLECULE TYPE: protein US-08-996-139-11
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US-08-996-139-11
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    Matches
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                         TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPOTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5 ·
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
**TOTATACK MINUSED: 118./08/0966.130
                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22 DECEMENT OF APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQLVQYIYKYTSYPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYPD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL
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    65;
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  Conservative
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                    23.6%;
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  37;
                  Score 235.5; DB 3; Pred. No. 3.1e-17;
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  Mismatches
  67;
                                    Length 294;
  Indels
  53;
Gaps
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Patent No. 6242213
GENERAL INFORMATION:
Matches
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh.
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                           -995-659-11
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: USSN 08/813,509 FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 22 DEC
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                                                                                                                              TOPOLOGY:
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                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKISNWTLSNGKLRVNQD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK
 65;
                                                                                                                                           amino acid
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                                                                                                                                                            294 amino acids
                                                                                                                                                                                                                  (206)233-0644
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 Conservative
                                                                                                                              linear
                                                                                                                                                                                                                                   (206)587-0430
                                                                                                          protein
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14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMBER: US/08/995,659
22 DECEMBER 1997
                23.6%;
 37;
Score 235.5;
Pred. No. 3.1e
37; Mismatches
                                                                                                                                                                                                                                                                      2852-A
                  .1e-17;
                                   DB 4;
                                   Length
 Indels
                                     294;
 53;
 Gaps
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release
CURRENT APPLICATION NUMBER: US/08
APPLICATION NUMBER: US/08
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 184v CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
 271
                                                                        211
                                                                                                                                         161 AQPEAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQD 210
                                                                                                                                                                                                                  107
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                                   149 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 190
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: ami
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                                                                                                                                                                               34 ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 89
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GFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFH
                                                                                                                                                                                                                  SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE
                                                                                                          GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG 148
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---STVQEKQQNISPLVRERGPQRVA----
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                                                                                                                                                                                                                                                                                                        Score 235.5; DB Pred. No. 3.5e-17
                                                                                                                                                                                                                                                                                       Mismatches
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Indels Length 316;

53;

Gaps 33

7;

270

US-08-989-362-2

Dirk M.

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RESULT 14
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mattson,
                                                                                                                                 271 FYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                211 GFYYLYANICFRHHETSGSVPTDYLQLMYYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFH 270
                                                                                                                                                                                                                                                                                                                                   107 SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE 160
                                                                                                                                                             149 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 190
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                                                                                                                                                                                                                                                                                                 34 ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 89
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 13-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                  GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG 148
                                                                                                                                                                                                                                                                                                                                                                     65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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13-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .Mammalian Cell Surface Antigens; Related
                                                                                                                                                                                                                                                                                                                                                                                                                      23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reagents
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                                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 235.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
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RESULT 15
US-08-995-659-13
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                                                                                                          Sequence 13, Appli
Patent No. 6242213
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: .34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
             APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: USSN FILING DATE: 23 DECEMBER ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0:
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
 NUMBER OF SEQUENCES:
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STREET: 5.
TTY: Seattle
                                                                                                                                                                                                                                                          153 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 190
                                                                                                                                                                                                                                                                                               216 LYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSI 275
                                                                                                                                                                                                                                                                                                                                                                      166 AHLT----INATDIPSGSHKVSL----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYY 215
                                                                                                                                                                                                                                                                                                                                                                                           34 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
COMPUTER: Ap
                                                                                                                                                                                                                                                                                                                                 94 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Apple Operating S SOFTWARE: Microsoft Word for Power
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                     NVGGFFKLRSGEEIŚIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perkins, Patricia Anne
RATION NUMBER: .34,693
                                                                                                                           Application US/08995659
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Galibert,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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22 DECEMBER 1997
Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%; Score 232.5; 32.9%; Pred. No. 7.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
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6.0.1
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Search completed: October 1, 2001, 11:43:33 Job time: 109 sec
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PRIOR APPLICATION DATA:

APPLICATION UNMBER: USSN 08/772,330

PILING DATE: 23 DECEMBER 1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

ANDE: Perkins, Patricia Anne
REGISTRATION UNMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430

TELEFAX: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.3%; Score 232.5; DB 4; Length 317; Best Local Similarity 32.9%; Pred. No. 7.2e-17; Matches 52; Conservative 33; Mismatches 62; Indels 11
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                     STREET: 51 Seattle
                                                                                                                                         153 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 190
                                                                                                                   276 NVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                216 LYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSI 275
                                                                                                                                                                                                                                        COUNTRY: UP
ZIP: 98101
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Maximum DB seq length:
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SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:

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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen
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AAW27137
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                                                           Tumour necrosis fa
Human Apoptosis in
Human Apoptosis in
Human apoptosis in
Novel cytokine Apo
Human TL2 protein.
Human TRAIL polype
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                    Human Apo-2 ligand 
Protein associated
AGP-1.
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AAB67248	8441	AAY84418	AAY91024	AAY17874	AAW59654	AAW83017	AAW83194	AAW68292	AAW69956	AAW83019	AAB08275	AAB28695	AAB28694	AAW44353	AAW56762	AAW19788	AAY01518	AAY71985	AAB08274	AAB28693	AAY88630	AAY27019	AAB28692	AAY27018	AAY27017	AAY27016	AAY01516	AAB50977	AAB67243	AAB48350	AAY81956	0854	AAB24038
Human RANKL. Homo	Amino acid sequenc	acid	Mouse OBM protein	Murine TRANCE. Mu	Amino acid sequenc	Osteoclastogenesis	Human osteoprotege		NF-kB receptor act	a	quen	muAGP-1 (120-2	Fc-muAGP-1 (99-291	Murine AGP-1. Mus	Murine TRAIL polyp	Mouse apoptosis in	æ	regi	Ω. 	AGP-1	acto	ង	AGP-1	Apo-2	Apo-2	Ą	in associate	PRO10	Apo2 ligand	TL2 po	Apo-2	acid sec	Human PRO1096 prot

## ALIGNMENTS

RESULT AAW76332

AAW76332;

AAW76332 standard; Protein;

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TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation; arthritis; septicaemia; transplant rejection; autoimmune disease inflammatory bowel disease; graft versus host disease; infection stroke; ischaemia; acute respiratory disease syndrome; psoriasis restenosis; brain injury; AIDS; bone disease; cancer; atherosclerosis; Alzheimer's disease; human; therapy; diagnosis;
WPI; 1998-497862/43.
                    Lyn SDP,
                                                                 28-JUL-1997;
05-FEB-1997;
                                                                                                  04-FEB-1998;
                                                                                                                                               EP867509-A2.
                                                                                                                                                                                                                                                                                  Human TL2 (TRAIL), ligand for TR5.
                                                                                                                                                                                                                                                                                                       11-JAN-1999 (first entry)
                                         (SMIK)
                                                                                                                         30-SEP-1998.
                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                           Ligand.
                                          SMITHKLINE BEECHAM CORP.
                     Tan KB,
                                                                  97US-0901469.
97US-0795910.
                                                                                                  98EP-0300827
                    Truneh A,
                     Young PR;
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infection;
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AAW95032
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Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist to the polypeptide activity comprises administering an antagonist to the polypeptide conclectide sequence encoding the polypeptide for its ligand, polypeptide that competes with the polypeptide for its ligand, substrate or receptor. The active agents can be used for the substrate or receptor. The active agents can be used for the substrate or receptor. The active agents can be used for the substrate or receptor. The active agents can be used for the substrate or receptor. The active agents can be used for the substrate or receptor. The active agents can be used for the substrate or receptor. The active agents can be used for the substrate or receptor. The active agents concerned to the polypeptide for its ligand, substrate or receptor. The active agents cancer disease, infection, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, particular, inflammatory bowel disease, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disease), atheroscelerosis and Alzheimer's disease.
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Best Local :
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                                                                                                  EP897114-A2
                                                                                                                                                                                                                                acute respiratory athersclerosis; Al
                                                                                                                                                                                                                                                                                              inflammation; septicemia; autoimmune disease; transplant rejection;
graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
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                                        17-FEB-1999
                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95032 standard;
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's disease.
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Pred. No. 3.4e-94;
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RESULT
AAW27134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying agonists or antagonists to tumour concerns factor receptor (TNN-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (1) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (11) contacting TL2 or TL4 with a candidate compound in the presence of TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, contentions stroke, ischemia, acute respiratory disease syndrome, the present sequence represents a TNF-R related polypeptide TL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1997;
13-AUG-1997;
26-AUG-1997;
                                           Apoptosis inducing molecule-I; AIM-I; autoimmune tumour necrosis factor ligand superfamily; AIM-I neoplasia inhibition; anti-inflammatory agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) useful for treating stroke, Alzheimer's disease and AIDS
                                                                                                                                          02-APR-1998
                                                                                                                                                                                                        AAW27134 standard; Protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14-15; 18pp; English.
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                                                                                                                                                                                                                                                                                                                   EASFFGAFLVG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \verb|milrtseetistvqekqqnisp|| vergpqrvaahitgtrgrsntlsspnsknekalgrk|
                                                                                                                                                                                                                                                                                     easffgaflvg 279
                                                                                                                                                                                                                                                                                                                                                                                                                in swess rsghsflsnlhlrngel vihekgfyyiysqtyfrfqeeikentkndkqmvqyi
                                                                                                         Apoptosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                         (first entry)
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97US-0055513.
97US-0056980.
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                                                                                                         inducing
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                                                                                                         molecule-I
                                                                                                           (AIM-I).
                                                             altered expression;
                                                                            disorder;
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                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               angioimmunoproliferative lymphadenopathy (AII), rheumatoid arthritis, diabetes, and multiple sclerosis, graft versus host disease, to inhibit neoplasia such as tumour cell growth, to treat restenosis, to regulate haematopoiesis in endothelial cell development, to stimulate peripheral tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be used for treating cachexia, cerebral malaria, rheumatoid arthritis or osteoporosis, for preventing graft-host rejection, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human Apoptosis inducing molecule-I (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand superfamily. The products can be used in the diagnosis and treatment disorders related to under-expression, over-expression or altered expression of AIM-I. AIM. I or agonists can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated apoptosis inducing molecule-I - used to develop products for the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft versus host disease or inflammation.
Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
                    Human apoptosis inducer cytokine TRAIL.
                                                                                                                                                                                                                                                                                                                                                                             anti-inflammatory agents, for treating endotoxic shock or to prevent {\tt activation} of {\tt HIV}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-470807/43.
N-PSDB; AAT85210.
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                                                                                 AAW19787 standard;
                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoproliferative disease lymphadenopathy (IPL),
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191; Conserv
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                    Score 996; DB 18;
Pred. No. 3.4e-94;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAIL, a novel cytokine, induces apoptosis in cancer a virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral infection and for us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10;
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29-JUN-1995;
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thrombotic microangioplasty; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                               YKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH 180
EASFFGAFLVG
                                                                                                                    INSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYI 120
                                       y ky tsypd pill \texttt{m} ks \texttt{arnscw} s k \texttt{dae} y \texttt{glysiy} q \texttt{ggifelkendrif} v \texttt{svtnehlid} \texttt{m} \texttt{dh} \texttt{h}
                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       281
                                                                                                                                                                                                                                                                                           100.0%; llarity 100.0%; Conservative 0
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89..90
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/note= "contains a receptor-binding region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "potential KEX2 protease processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "potential KEX2 protease
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Pred. No. 3.4e-94;
); Mismatches 0;
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ID AAW1
A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental cDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays.
Sequence
                                                                                                                                                         Claim 4; Fig la; 72pp; English.
                                                                                                                                                                                 Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce apoptosis for the treatment of breast and colon cancer
                                                                                                                                                                                                                 N-PSDB; AAT72796
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                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
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                                                                                               This sequence represents the human tumour necrosis factor (TNF)-relative receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acu
                   rejection, graft vs. host disease, infection, stroke, ischaemia, erespiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers dispute the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF; TL2.
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 32-33;
                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding tumour necrosis factor receptor TR6 - polypeptide, antibody, agonist, antagonist, etc
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14-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             easffgaflvg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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97US-0041230.
97US-0853684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor-related apoptosis-inducing ligand
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                                                                                                                                                                                                                                                                                                                                     34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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hes 0;
                        and Alzheimers disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                    (TNF)-related
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                                                                                                       acute
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                     25-JUN-1996;
29-JUN-1995;
01-NOV-1995;
apoptosis of Jurkat cells.
                                                     DNA encoding cytokine TNF-related apoptosis ligand polypeptides useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW56760 standard; Protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
          This represents a human tumour (TRAIL) polypeptide. The human
                                                                                                                    Goodwin RG,
                                                                                                                                   ( VMMI)
                                                                                                                                                                                           25-JUN-1996;
                                                                                                                                                                                                            09-JUN-1998
                                                                                                                                                                                                                              US5763223-A.
                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         cytokine;
                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inswessrsghsflsnlhlrngelvihekgfyyiysqtyfrfqeeikentkndkqmvqyi
                                                                                                                                                                                                                                                                                                                                                                  TRAIL
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                                                                                                                                    IMMUNEX
                                                                                           AAV29518
                                     Columns
                                                                                                                                                                                                                                                                                                                                        therapy;
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                                                                                                                                                                                                                                                                                                                                                                  polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                   Wiley SR
                                                                                                                                                     96US-0670354.
95US-0496632.
95US-0548368.
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                                                                                                                                                                                          96US-0670354
                                                                                                                                     CORP.
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                         /note=
39..28:
                                                                                                                                                                                                                                                                          /note=
19..38
                                     33-36;
                                                                                                                                                                                                                                                                                                                                         leukaemia; lymphoma; melanoma; viral infection.
The human cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                 "transmembrane region"
                                                                                                                                                                                                                                               "extracellular domain"
                                                                                                                                                                                                                                                                                  "N-terminal cytoplasmic domain"
                                    28pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 996; DB 19;
Pred. No. 3.4e-94;
                                    English
necrosis factor related apoptosis ligand
and murine TRAIL polypeptides can induce
encoding nucleic acid sequences are usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Best Local
The present sequence represents human AGP-1. AGP-1 is a tumour-necrosi factor (TNF) related protein, involved in inflammation, myelopolesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) describe in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay reagents for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to regulate AGP-1 expression and antagonistic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells (e.g. to isolate antigens for vaccine development). The polypeptides ce used to treat leukaemia, lymphoma or melanoma (e.g. by extracorpore treatment of blood or bone-marrow), or to treat viral infections.
                                                                                                                                                                         WPI; 1998-042194/04
N-PSDB; AAV15295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW44354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                 Claim 7; Page 36-37;
                                                                                                                          haematopoietic
                                                                                                                                 Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein useful for treating inflammation, bone resorption a
                                                                                                                                                                                                             Danilenko
                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                     06-JUN-1997;
                                                                                                                                                                                                                                                                                                             11-DEC-1997.
                                                                                                                                                                                                                                                                                                                                      WO9746686-A2
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human AGP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW44354 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for producing the recombinant TRAIL polypeptides, which may be useful
                                                                                                                                                                                                                                     (AMGE-) AMGEN
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|||||||||||
| easffgaflvg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191;
                                                                                                                                                                                                                                                                                                                                                                                                  AGP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                             DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                     bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                    tumour necrosis factor-related protein; TNF; bone resorption; haematopoietic disease.
                                                                                                                          diseases
                                                                                                                                                                                                             Johnson
                                                                                                                                                                                                                                                              96US-0660562
                                                                                                                                                                                                                                                                                     97WO-US09895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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                                                                                                54pp; English.
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                                                                                                                                                                                                             Simonet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 996; DB 19;
Pred. No. 3.4e-94;
Mismatches 0;
                                                                                                                                    inflammation, bone resorption and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                       AGP-1 is a tumour-necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Best Local S
Matches 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus erythematosus, psoriasis, scleroderma, infection-related inflammation) or bone resorption diseases (e.g. osteoporosis, osteomyelitis, pypercalcaemia, Paget's disease). AGP-1 can be used to treat haematopoietic diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA, are used to produce recombinant AGP-1.
                           Claim 1; Fig 1A; 86pp; English.
                                             A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis in mammalian cancer cells
                                                                                                                                                                                                                      W09936535-A1
                                                                                                                                                                                                                                                                        Cytokine;
                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                            24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                AAY27012 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                      15-APR-1998;
15-JAN-1998;
                                                                                                                Ashkenazi AJ,
                                                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                  15-JAN-1999;
                                                                                                                                                                                                                                                           lupus; immune-mediated glomerular nephritis; human
                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                           1999-444397/37.
DB; AAX86987.
                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         EASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191;
                                                                                                                                                                                                                                                                                       Apo-2 ligand (Apo-2L)
                                                                                                                                                                                                                                                                    Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                    98US-0060533
98US-0007886
                                                                                                                Kelley
                                                                                                                                                                                  99WO-US01039
                                                                                                                                                                                                                                                                                                                                                                                                                191
                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                 RF,
                                                                                                                                                                                                                                                                                       polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 996; DB 19;
Pred: No. 3.4e-94;
; Mismatches 0;
                                                                                                                 MT,
                                                                                                                  Pitti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                      disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                    270
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This

This sequence (Apo-2L). The

represents a novel Apo-2L polypeptide

can be

e produced

designated *i* by standard

Apo-2

The specification describes the use a polypeptide corresponding to at least the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases

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RESULT 1
AAY01517
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immunemediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis.
                                                                                Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also use prevention or treatment, and similar use of corresponding ligations.
                                                                                                                                                                                                                                                                                                                                surface receptor;
                                               Claim
                                                                                                                                    WPI; 1999-156177/14.
                                                                                                                                                           Belliveau JF,
                                                                                                                                                                                                           04-AUG-1997;
                                                                                                                                                                                                                                  04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                            Neurodegenerative disease; autoimmune disease; lupus erythematosus; rhuematoid arthritis; SEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY01517 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                Protein associated with neurodegenerative and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-1999
                                                                                                                                                                                 (INMR ) BIO MERIEUX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | EASFFGAFLVG
||||||||||
| easffgaflvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFYSVTNEHLIDMDH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     milrtseetistvqekqqnisplvrergpqrvaahitgtrgrsntlsspnsknekalgrk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ykytsypdpillmksarnscwskdaeyglysiyqggifelkendrifvsvtnehlidmdh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191;
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                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                              13;
                                                                                                                                                           Perron
                                                                                                                                                                                                           97FR-0010176
                                                                                                                                                                                                                                   97FR-0010176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281
                                                                                                                                                                                                                                                                                                                                TRAIL protein
                                           21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                           Ħ,
                                               French.
                                                                                                                                                           Rieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 996; DB 20;
Pred. No. 3.4e-94;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         inflammatory disease;
                                                                                                                                                                                                                                                                                                                                              apoptotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                  o useful
ligand a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local S
Matches 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of degenerative, autoimmune and inflammatory diseases. The polypeptides can be used in treatment of neurodegenerative disease, lupus erythematosus, rhuematoid arthritis, and SEP. The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and a therapeutic target, e.g. its apoptotic activity can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that binds to specific receptors, inhibiting formation of natural complex.
            Claim
                                                                                                                                                                                                                                                                                          antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular diseas;
                                             rusion protein of AGP-1 protein proliferative disorders, immune
                                                                                                                                                                                                                                   WO200063253-A1.
                                                                                                                                                                                                                                                                                arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                             AAB28691;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB28691 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                 N-PSDB;
                                                                                                                                        (AMGE-)
                                                                                                                                                               16-APR-1999;
                                                                                                                                                                                      24-MAR-2000; 2000WO-US08004
                                                                                                                                                                                                            26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                Human AGP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRK
                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYI 120
                                                                                2000-665240/64.
DB; AAC67831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            easffgaflvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               milrtseetistvqekqqnisplvrergpqrvaahitgtrgrsntlsspnsknekalgrk 150
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                                                                                                                                                                                                                                                                                                                                       AGP-1; type II transmembrane protein; cytostatic; antiviral;
                                                                                                                 Meng
          Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
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             2;
                                                                                                                                                                                                                                                                                                                                                                                      (first
            93pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 281
                                                                                                                                                                                                                                                                                                                                                                                     entry)
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             English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 996; DB 20;
Pred. No. 3.4e-94;
                                             and an Fc region, used to trea
disorders, and virally-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281;
                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
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RESULT 1
AAB24038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                          08-MAR-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human AGP-1, a type II transmembrane protein. Fusion proteins comprising an FC immunoglobulin region fused to the N-terminal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies.
Antibodies specific the growth of tumors
                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                             Human PRO1096 protein sequence SEQ
                                    N-PSDB;
                                                                   Botstein D,
                                                                                                                                                                                    02-DEC-1999;
                                                                                                                                                                                                                                WO200053750-A1
                                                                                                                                                                                                                                                                                                                                     25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                           AAB24038;
                                                                                                                                                                                                                                                                                                                                                                                 AAB24038 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                            identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EASFFGAFLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                       easffgaflvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          milrtseetistvqekqqnisplvrergpqrvaahitgtrgrsntlsspnsknekalgrk 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191;
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                                    AAC58120
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                                                                    Goddard
                                                                                                                          99WO-US20111.
99US-0162506.
99WO-US28313.
                                                                                                                                                                                                                                                                                      diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                99WO-US28634
                                                                                                                                                            99WO-US05028
                                                                                                                                                                                    99WO-US28551.
                                                                                                                                                                                                                                                                            tumourigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              191
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                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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s in
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 PRO polypeptides, used to diagnose and mammals, and to identify inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0%;
                                                                    Gurney
                                                                                                                                                                                                                                                                                      neoplastic disease;
                                                                                                                                                                                                                                                                                                                                                                                 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 996; DB 21;
Pred. No. 3.4e-94;
                                                                   ΑL,
                                                                                                                                                                                                                                                                            anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                             IJ
                                                                   Roy
                                                                                                                                                                                                                                                                                                             NO:51.
                                                                    MA,
                                                                                                                                                                                                                                                                            e; proliferation; detection.
                                                                    Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                      Wood
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                                                                                                                                                                                                                                                                                        cancer;
  inhibit
PRO
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                                                                      WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270
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AABO8545
ID AABO
XX AABO
AC AABO
DT 20-D
XX Huma
KW Huma
KW TRAI
KW TRAI
KW NOO!
OS HOMO
OS HOMO
XX WO20
PN WO20
XX 15-F
XX 15-F
XX Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an antibody that binds to a human CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; CC PRO3434; PRO1927; PRO3567; PRO1293; PRO1303; PRO43344; PRO4354; CC PRO4397; PRO1959; PRO1555; PRO1296; PRO1303; PRO43644; PRO4354; CC anticancer activity and can be used to diagnose tumours in mammals, by Cd detecting complex formation when the antibody is contacted with test CC cells: Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), CC especially the antibodies, or an antisense oligonuclectide which hybridises to genes encoding (I), can be used to inhibit tumour growth, CC preferably by inducing cell death. Methods from the present invention CC can be used to identify compounds which inhibit the biological activity CC of (I). AAC58102 represent PC primers and hybridisation CC probes used in examples from the present invention for human PRO compounciectide and protein sequences given in the exemplification of the propersent invention for human PRO compounciectide and protein sequences given in the exemplification of the propersent invention for human PRO compounciectide and protein sequences given in the exemplification of the propersent invention for human PRO compounciectide and protein sequences given in the exemplification of the propersent invention for the present invention for the present invention for human PRO compounciectide and protein sequences given in the exemplification of the present invention for the present invention for the present invention for human PRO compounciectide and protein sequences given in the exemplification of the present invention for the present invention for the present invention for human PRO compounciectide and protein sequences given in the exemplification of the present invention for the present invention for the present invention for human protein sequences given in the present invention for human protein sequences given in the present invention for huma
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Best Local Similarity
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                     (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                           24 - AUG - 2000
                                                                                                                                                                                                           WO200048619-A1
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                 non-small cell
                                                                                                                                                                                                                                                                                                                      TRAIL receptor
                                                                                                                                                                                                                                                                                                                                         Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide; TNF related apoptosis-inducing ligand; tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a human TRAIL polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB08545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB08545 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                  16-FEB-1999;
                                                                                                             15-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide activity or expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271
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                                                                                                                                                                                                                                                                                                                      related apoptosis-inducing ligand; tumour confirmation receptor ligand; solid tumour; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotide and protein sequences given in the exemplification present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              milrtseetistvqekqqnisplvrergpqrvaahitgtrgrsntlsspnsknekalgrk 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 AA;
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                                                                                                                2000WO-US03891
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                 Lung
                                                                  99US-0120313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                   carcinoma
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Best Local Similarity 100.0%;
Matches 191; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human TRAIL (tumour necrosis factor (TNF) related apoptosis-inducing ligand) polypeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a synergistic mixture of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is synergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Killing of tumour cells, e.g. solid tumours or carcinoma, administration of synergistic combination of diterpenoid cumour necrosis factor related apoptosis-inducing ligand.
                        Kim KJ,
                                                                                                                                            09-JAN-1996;
                                                                                                                                                                                                    08-JAN-1997;
                                                                                                                                                                                                                                                                   04-APR-2000
                                                                                                                                                                                                                                                                                                                              US6046048-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Apo-2 ligand protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-558253/51
N-PSDB; AAA64325.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; apoptosis; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo-2 ligand;
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                                                                                 (GETH ) GENENTECH INC.
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                        Ashkenazi AJ,
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                                                                                                                                            96US-0009755
                                                                                                                                                                                                    97US-0780496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoclonal antibody; hybridoma cell line; diagnosis;
                        Chuntharapai A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
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Pred. No. 3.4e-94;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ligand, e.g. 200,
Apo-2 ligand serum,
                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2; antiinflammatory; immunosuppressive; cerebroprotective; vasotropic; antiastbmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; nootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Fig la; 46pp; English.
                                  12-JUN-2000; 2000WO-US16134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB48350 standard; Protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated monoclonal antibodies having antigen specificity for Apo-2 ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo-2 ligand serum, and for treating diseases associated with increased
                                                                                                    21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human TL2 polypeptide.
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                                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EASFFGAFLVG 191
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Pred. No. 3.4e-94;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a human tumour necrosis factor (TNF) related receptor, TR6. TR6 can be expressed by standard recombinant methodology. The TR6 polypeptides are useful for treating chronic and acute inflammation, rheumatoid arthritis, septicemia, autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor necrosis factor related receptor TR6 polynucleotides and polypeptides useful for e.g. for treating chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, infection cancer, bone diseases
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N-PSDB; AAC84745.
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sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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11	144.5	14.5	216	11	070332
12	135	13.6	217	11	Q9ERG6
13	131.5	13.2	232	11	035853
14	126.5	12.7	225	13	Q9IB42
15	122.5	12.3	205	4	Q9UKS8
16	122	12.2	232	4	Q9UIV3
17	121.5	12.2	225	13	Q9IB41
18	121.5	12.2	246	13	091976
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9.4	9.4	9.7	10.4	10.4	10.5	10.7	11.0	11.0	11.0	11.0	11.0	11.3	11.4	11.4	11.4	11.5	11.5	11.6	11.6	11.7	12.0	12.0	12.0	12.1	12.2
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## ALIGNMENTS

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144 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 188       : :   :  :  : :::::::::::::::::	85 VIHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 143 : :     :      : 106 RVPQDGRYYLYSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQLLKGVGTKCWAP 165	30 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 84	Query Match 30.7%; Score 305.5; DB 13; Length 214; Best Local Similarity 37.6%; Pred. No. 1.2e-19; Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps	LT 1  Z5  Z9DDZ5  PRELIMINARY; PRT; 214 AA.  Q9DDZ5;  01-MAR-2001 (TrEMBLrel. 16, Created)  O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)  O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)  TRAIL-LIKE PROTEIN.  Erachydanio rerio (Zebrafish) (Zebra danio).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  Cypriniformes; Cyprinidae; Rasborinae; Danio.  NCBI_TAXID=7955;  [1]  SEQUENCE FROM N.A.  Bobe J. Goetz F.W.;  Bobe J. Goetz F.W.;  Molecular cloning and expression of a TNF receptor and two TNF  ligands in the fish ovary.  Comp. Biochem. Physiol. 0:0-0(2001).  EMBL; AF250041; AA647640.1;  SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

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01-OCT-2000 (TrembLrel. 15,
01-MAR-2001 (TrembLrel. 16,
RECEPTOR ACTIVATOR OF NF-KB
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EMBL; AB022036; BAA36970.1;
EMBL; AB022037; BAA36970.1;
EMBL; AB022038; BAA36970.1;
INTELPPO; IPR000478; -.
                                                         "Receptor activator of NF-kB ligand Submitted (SEP-1999) to the EMBL/GerEMBL, AB032771; BAA97257.1; -
                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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Gene 230:121-127(1999).
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Mammalia; Eutheria;
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  PROSITE;
                      InterPro; IPR000478; -. Pfam; PF00229; TNF; 1.
                                                                                                                             Ikeda T.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=10090;
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"Cloning and characterization
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PS50049; TNF_2; 1.
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156
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RESULT CASE OF THE PROPERTY OF
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Best Local S
Matches 62
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Best I
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Q9JJK8;
Q1-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Mus musculus (Mouse).
"-rvota; Metazoa; Chordata;
"-rvota; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003263; -.

Pfam; Pd229; TNF; 1.

ProDom; PD008600; -; 1.

PROSITE; PS50049; TNF_2; 1.

SEQUENCE 199 AA; 22150 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1999) to the EMBL; AB032772; BAA97258.1; InterPro; IPR000478; -. InterPro; IPR003263; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Somatostatin, a new RANKL isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikeda
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173
                                      168
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Local :
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                                                                                                                                                                                                                                                                                                    VQEKQQNISPLVRERGPQRVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEETI-----STVQEKQQNISPLVRERGPQRVA---------
IQVSNPSLLDPDQDATYFGAFKV
                                    VSVTNEHLIDMDHEASFFGAFLV
                                                                                 VPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEIS
                                                                                                                   NTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIF
                                                                                                                                                                                            PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQPFAHLT-'---INAASIPSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE
                                                                                                                                                                        PSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGS
                                                                                                                                                                                                                                                              VQKELQHIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T., Takahashi H.,
                                                                                                                                                                                                                                                                                                                                                62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) (TrembLrel. 15, 0) (TrembLrel. 15, 1) (TrembLrel. 16, 1) (TrembLrel. 16, 1) TIVATOR OF NF-KB I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
A
                                                                                                                                                                                                                                                            -GPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT-----INAASI
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                                                                                                                                                                                                                                                                                                                                                                    23.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 235.5;
Pred. No. 2.8e
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                      190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoblast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          401C13EB5E8CE166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8B2CE8E4C7B534CC CRC64;
                                                                                                                                                                                                                                                                                                                                                Mismatches
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nes 65;
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?.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
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                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Loc
Matches
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Q9ESE2;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                01-OCT-2000
01-OCT-2000
01-MAR-2001
FAS LIGAND.
    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY
Kirii Y., Inoue T., Yoshino K.;

Kirii Y., Inoue T., Yoshino K.;

"Cynomolgus monkey Fas ligand mRNA, complete cds
"Cynomolgus monkey Fas ligand wRNA, complete cds
                                                                                                                                                          Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopith
                                                                                                                                                                                                         PT-FASL OR CM-FASL OR RM-FASL.
Macaca nemestrina (Pig-tailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, sequence and functional characterization homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186(2000).

EMBL; AF187319; AAG17031.1; -.
SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, RECEPTOR ACTIVATOR OF NF-KB
                                                                                                                                      Cercopithecinae;
NCBI_TaxID=9545;
                                                                                                                                                                                                                                                                                           91XW6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
 Submitted
                                                                                         Kirii Y.,
                                                                                                    SPECIES=M.nemestrina;
                                                                                                                                                                                                                                                                               Q9MYL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
PubMed=11092398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                "Pig-tailed monkey Fas ligand mRNA,
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQEKQQNISPLVRERGPQR---VAAHITGT-----RGRS-----NTLSSPNSKN'53
                                                                                                                                                                                                                                                                                                                                                   PSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                              KVSL---
                                                                                                                                                                                                                                                                                                                                                                                                LQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISVQVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQRELQHIV-----GPQRFSGVPAMMEGSWLDVARRGKPEAQPFAHLTINAADIPSGSH
                                                                                                                                                                                            nemestrina (Pig-tailed macaque), fascicularis (Crab eating macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tan J., Huang L.,
  (NOV-1999)
                                                                   (NOV-1999)
                                                                                         Inoue T.,
                                                                                                                                                                                                                                           0 (TrEMBLrel.
0 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              -SSWYHDR-GWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPADY
                                                                                                                                       Macaca.
9541, 9544;
                                                                                         a; STRAIN=PIG-TAILED MONKEY; Yoshino K.;
                                                                   to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.3%;
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16,
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  the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao X.H.,
                                                                                                                                                                                                                                            Created)
Last sequence Last anno
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Last an
LIGAND.
nd mRNA, complete cds.";
EMBL/GenBank/DDBJ databases.
                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 232.5; DB 1
Pred. No. 5.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4B87A4D706AD098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence up
annotation
                                                                                                                                                                                                                                             sequence up
annotation
                                                                                complete cds.";
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                                                                                                                                                                                                                                                                                           280
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                                                                                                                                                             Cercopithecidae;
                                                                                                                                                                                              (Cynomolgus monkey), and
                                                                                                                                                                                                                                                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Rat
                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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PART OF THE REPORT OF THE REPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WV90;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
FAS LIGAND (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO00478; -. Pfam; pr00229; TNF; 1.
Pfam; pr00229; TNF; 1.
PRINTS; pr01234; TNECROSISFCT.
PROSITE; pS00251; TNF_1; 1.
PROSITE; pS50049; TNF_2; 1.
SEQUENCE 280 AA; 31367 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [3]
SEQUENCE FROM N.A.
SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;
SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;
Kirii Y., Inoue T., Yoshino K.;
Rhesus monkey Fas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035140; BAA90294.1; -.
EMBL; AB035138; BAA90294.1; -.
EMBL; AB035139; BAA90295.1; -.
                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                        chronic woodchuck viral hepatitis."; Clin. Exp. Immunol. 0:0-0(1999). EMBL; AF152368; AAD38387.1; -.
                                                                                                                                                        SMART; S
                                                                                                                                                                                               Pfam; PF00229; TNF; 1.
PROSITE; PS00251; TNF_1;
PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                       TISSUE-HEALTHY LIVER;
Hodgson P.D., Grant M.D., Michalak T.
Perforin and Fas/Fas ligand-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marmota.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9WV90
                                                                                                                                                                                                                                                                     InterPro; IPR000478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FFGAF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKYPQDLVMMEGKMMS-YCTTGQMWAHSSYLGAVFNLTSADHLYVNVSELSLVNFEESQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSQKHTASSLEKQIGHPSPPPEKKEQRKVAHLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDT-YGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQ-----SCTNLPLSHKVYMRN 214
                                                                                                                                                                             SM00207; TNF;
ch 17.3%; l Similarity 28.4%; 52; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 (TrEMBLrel. 12,
9 (TrEMBLrel. 12,
1 (TrEMBLrel. 16,
                                                                                                             169
                                                                                                                                     169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              N.A.
                                                                                                             AΑ;
                                                                                                                                     169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                             19274
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27.0%;
                                                                                                                                                                                                                                                                                                                                                                                 Michalak T.I.;
                                                                                                             WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 183; DB
Pred. No. 1.3e
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
Score 172; DE
Pred. No. 6.5e
95; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Eu
Sciurognathi; Sciuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                             FDE395B014717B6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F0B284D61A132EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
                                                                                                                                                                                                                                                                                                                                                            cytotoxicity
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DB 11;
.5e-08;
es 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
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                                     Length 169;
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                            acute
  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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RESULT 095150 O9 AC O9 DT 01 DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 53
                       095150;
095150;
01-MAY-1999
01-MAY-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tregaskes C.A., Young J.R., Burnside J.;
"Cloning of a putative chicken CD40 ligand.";
Submitted (JUN-199) to the EMBL/GenBank/DDBJ
EMBL; AJ243435; CAB95748.1; -.
Interpro; IPR000478; -.
Pfam; PF00229; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 272 AA; 30862 MW; 5409F24A8E53CCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Garronta: Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
PUTATIVE CD154 (CD40 LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN LINE 0; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q918D8;
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                                                                                                                                                                                                        175
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                                                                                                                                                                                                                                                                                                      150
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                                                                                                                                                                                                                                                                                                                                                               RTASEELPKFEMHRSHEHPHLKSRNETSVAEEKRQPIATHLAGV--KSNTTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVNVNPGNTYFGMF
                                                                                                                                                                                                      LIDMDHEASFFGAF
                                                                                                                                                                                                                                      PFTLYIYLYLPMEEDRLLMKGLDTHSTS-TALCELQSIREGGVFELRQGDMVFVNVTDST 256
                                                                                                                                                                                                                                                       QMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEH
                                                                                                                                                                                                                                                                                                  RTSEETISTVQEKQQNISPLVRERGP-----QRVAAHITGTRGRSNTLSSPNSKNEK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSKYPQDLVLMEGKMMNYCTTGQMWAR-----SSYLGAVFNFTSNDHLYVNVSELSLI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDT-YGISLISGVKYQKGGLVINDTGLYFYYSKIYERGQ-----SCNNQPLSHKYYVK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-K 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNTEPSL----EKQIGHPSSPSDKKALRRAAHLT---GKPNSRSSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
                          (TrEMBLrel.
                                                         (TrEMBLrel.
                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neognathae;
                                                                                                                                                                                                        188
                                                                                                                                                                        270
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6%;
27.3%;
                         10,
                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence up
                         Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 165; DB
Pred. No. 4.9e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; 
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5409F24A8E53CCD7
                                                                                         174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
1.9e-07;
nes 77;
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                                      update)
                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                       RESULT
OPENING
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Best Local S
Matches 49
                         pathway.";
Submitted
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                                                                                                                                                                                                                                                                                                                                    LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156
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InterPro; IPR003636; -.

Pfam; PR00229; TNF; 1.

PRINTS; PR01234; TNECROSISFCT.

PRODOM; PD002012; -; 1.

PROSITE; PS50049; TNF_2; 1.

SMART; SM00207; TNF; 1.

SEQUENCE 174 AA; 20131 MW; (
                                                                                                                                                                                                                                                                                                                                                          Q9QYH9;
Q9QYH9;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                            SEQUENCE FROM N.A.

Tamada K., Shimozaki K., Chapoval A.I., Zhu G.
Ullrich S., Chen S.F., Sica G., Flies D., Hsie
Nagata S., Ni J., Chen L.;
"Modulation of cell-mediated immunity through
                                                                                                                                                                  TISSUE=FETAL LIVER CELL;
Misawa K., Nosaka T., Kitamura T., I
"Murine LIGHT, a homologue of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1997)
EMBL; AF039390; AAD0
HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSDE-VASCULAR ENDOTHELIAL;
Yu G.-L., Zhai Y., Ni J., Iruela-Arispė
Lu J., Kozak D., Jiang G.-W., Rojas L.,
Gentz S., Lippman M.E., Aggarwal B.B., R
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000478; -. InterPro; IPR003636; -. Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                  Submitted (JUN-1999)
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                           LIGHT PROTEIN (LIGAND FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiogenesis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu G.-L.;
"A Novel-Endothelial Cell-Specific Negative Regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKNDK--QM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVVITKVTDSYPEPTQLLMGTKSVC-----EVGSNWFQPIYLGAMFSLQEGDKLMVNVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHLIDMDHE-ASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WE-HELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISLVDYTKEDKTFFGAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
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49; Conservative
 (JAN-1999)
                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
(IN (LIGAND FOR HERPESVIRUS ENTRY MEDIATOR)
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Rodentia;
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Primates;
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                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
EMBL/GenBank/DDBJ
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Pred.
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                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Mismatches
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7.
                                                                                                                                                                                      Kojima
                                                                                                                                                                  Kojima T.;
LIGHT which
                                                                                                                                                                                                                                                                                                                                                                                                                              239
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                                                                 Zhu G.,
)., Hsieh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L., Huang W.-Q., Xing L.,
Janat M.F., Buergin M.,
Ruben S., Gentz R., Li L.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
'.8e-07;
                                                                                                                                                                                                                                                                       Muridae;
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                                 LIGHT
 databases
                                                                 Su J.,
S.L., 1
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Hsu H.,
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RESULT 11
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Best Local Similarity
Matches 47; Conserv
  Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLPEL 16, Last annotation update)
TUMOR NECROSIS FACTOR-ALPHA (FRAGMENT).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORCE W.R., Todd P.K., Mikayama T.;

Wouse LIGHT; Molecular Genetics, Ligand Binding and Expression.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB029155; BAA88559.1; -.

EMBL; AF227533; AAF76453.1; -.

EMBL; AF227533; AAF36722.1; -.

EMBL; AF227533; AAF36722.1; -.

HSSP; P01375; 4TSV.

InterPro; IPR000478; -.

Pfam; PF00229; TNF; 1.

PRNDTS; PR01234; TNECROSISFCT.

PROSITE; PS50049; TNF_2; 1.

SEQUENCE 239 AA; 26338 MW; 217874AC71AD6BE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98234044; PubMed-9573100; Melby P.C., Tryon V.V., Chandrasekar B., "Cloning of Syrian hamster (Mesocricetus analysis of cytokine mRNA expression in eleishmaniasis.";
                                                                                                                                                     NON_TER
                                                                                                                                                                                                                           PRINTS; PR01234; TNECROSISFCT PROSITE; PS00251; TNF_1; 1. PR0SITE; PS50049; TNF_2; 1.
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                                                                                                                                                                                                        SMART; SM00207;
                                                                                                                                                                                                                                                                                                           Pfam; PF00229; TNF; 1
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000478; -.
                                                                                                                                                                                                                                                                                                                                                           EMBL; AF046215; AAC
HSSP; P06804; 2TNF
                                                                                                                                                                                                                                                                                                                                                                                    Infect. Immun. 66:2135-2142(1998).
EMBL; AF046215; AAC40100.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus
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SEQUENCE FROM
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216 i
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23793
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                        14.5%;
                                                                                                                           MW;
     28;
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                        Score 144.5; DB : Pred. No. 2.4e-05
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Pred. No. 5.4e-06;
5; Mismatches 72;
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     Mismatches
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                                                  DB 11;
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     Indels
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                                                  216;
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  37;
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Gaps
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RESULT
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Best Local :
                                                                                                                       O35853;
O35853;
O1-JAN-1998
O1-JAN-1998
O1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF307013;
NON_TER 1
NON_TER 217
SEQUENCE 217 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbst M.M., Schountz T.; "Cloning of the deer mouse interferon gamma, interleukin-10 mecrosis factor genes."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF307013; AAG30264.1; -.
                                                                                                        01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2001 (TrEMBLrel. 16,
TUMOR NECROSIS FACTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
Peromyscus maniculatus (Deer mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ERG6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last amountation
                                                                                                 TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ERG6
MEDLINE=97246744; PubMed=9089109;
                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10042;
                        SEQUENCE FROM
                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUÉ=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peromyscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     161
                                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158
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                                                                                                                                                                                                                                                                                      106
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                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                    VNLLSAIKSPC-PKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLD
                                                                                                                                                                                                                                                           ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID 177
                                                                                                                                                                                                                                                                                                           HSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 129
                                                                                                                                                                                                                                                                                                                                                             ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINS-----WESSRSG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVNLLSAIKSPC-PKETPEGEELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMSLKDNQLVIPADGLYLVYSQVLFRGQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPQRVAAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS-------WESSRSGHSFLS
                                                                                                                                                                                                                                                                                     ALLANGMDLKDNQLVIPADGLYLVYSQVLFKGQ-----GCSNYVLLTHTVSRFAVSYEDK
                                                                                                                                                                                                                                                                                                                                     IGPOREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRRAN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK-----YTSYPD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPQREEKFPNPIIGSMGQTLTLRSSSQNSNDKPVGHVVANHQVEEQLEWLSHRANALLAN 108
                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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217
217
217
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                                                                                                                                                                        PRELIMINARY;
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                                                                                     (Mouse)
                        N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      217
23964 MW; · D6F90C74C0B3021F CRC64;
                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                   13.6%;
                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                       Last sequence up
                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                Score 135; DB 11;
Pred. No. 0.00017;
                                                           Craniata; Ver
Sciurognathi;
                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
                                                            Vertebrata;
thi; Muridae;
                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on update)
                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Sigmodontinae;
                                                           Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                               217;
                                                                                                                                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local S
Matches 41
                                                                                                  Matches
                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TUMOR NECROSIS FACTOR.
Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom.
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleosta
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9IB42;
Q9IB42;
                                                                                                                                                                                                    olivaceus.":

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB040448; BAA94969.1; -.

InterPro; IPR000478; -.

Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01234; TNECROSISECT PRODOM; PD002011; -; 1. PROSITE; PS00251; TNE_1; 1. PROSITE; PS50049; TNF_2; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                PRINTS; PR01234; TNECROSISFCT.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 225 AA; 24965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000478; -. InterPro; IPR003636; -. Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                    factor (TNF) cDNA and gene from Japanese plivaceus ".
                                                                                                                                                                                                                                                                                                                                             Pleuronectoidei; Bothidae;
NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U68414; AAB65593.1;
HSSP; P06804; 2TNF.
                                                                                                                                                                                                                                                                                          irono I., Nam B., Kurobe T., Aoki T.;
Characterization a
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strains."
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Cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenetics 45:459-461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 VKSPC-PKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
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                 72
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SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ-----EEIKENTKNDKQMVQY-IYKYT 124
                                                         EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPQRDEKFPNGLPLISSMAQTLSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPORVAAHITG---TRGRSNTLSSPNSKNEKALGRKINS-----WESSRSGHSFLSN 76
                                         EKTEPHNTLRQISSRAKAAIHLEG-RDEEDEETSENKLVWKNDEGLA-----FTQGGF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDLKDNQLVVPADGLYLVYSQVLFKGQ-----GCPDYVLLTHTVSRFAISYQEKVNLLSA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 AA;
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                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25513 MW;
                                                                                                            12.7%;
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23.0%;
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                                                                                                                                                                                                                                                                                                                                                             Paralichthys.
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                                                                                                            Score 126.5; DB Pred. No. 0.001;
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Pred. No. 0.00038;
5; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                   8F947FB25FC82658 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2ED6DA8E0DCAADD8 CRC64;
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225
                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei
                                                                                                                                                                                                                                                                             expression of tumor necrosis flounder Paralichthys
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                                                                                                                         DB 13;
                                                                                                78;
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                                                                                                Indels
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                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 232;
                                                                                                                                                                                                                                                                                                                                                                                       Neoteleostei;
                                                                                                31;
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                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
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Search completed: October Job time: 109 sec

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Best Local Similarity
Matches 43; Conser
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Q9UKS8;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                          PRINTS; PR01234; TNECROSISFCT.
PROSITE; PS00251; TNF-1; 1.
PROSITE; PS50049; TNF-2; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Rowen L., Madan A.,
Abbasi N., Dickhoff
Lasky S., Hood L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).

Homo sapiens (Human).

Chordata;
                                                                                                                                                                                                                                                                                                                          InterPro; IPR000478; -
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF129756; AAI
HSSP; P01375; 4TSV
                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYMPHOTOXIN ALPHA.
                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                     region."
                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
193
                      178
                                              135
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                    MDHEASFFGAF 188
                                                                                                                                                                TISTVQEKQQ------NISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDHEASFFGAF 188
LSPSTVFFGAF
                                              VQLFSSQYPFHVPLL-SSQKMVYPGLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPHLV-
                                                                    IYKYTS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLID 177
                                                                                            ---LWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSPKATSSPLYLAHE
                                                                                                                  KINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKOMVQY 119
                                                                                                                                            TPSAAQTARQHPKMHLAHSNLKP-----AAHLIGDPSKQNSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESLGTQVSLMSAVRSACQKSQEDAYRDGQGWYNAIYLGAVFQLNEGDKLWTETNMLSELE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SYPDPILLMKSARNSCWS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELVDN-----HIIIPRSGLYFVYSQASFRVSCSSDDADDGKEAAEKHLTSISHRVWLFT
                                                                                                                                                                                                                                                   205 AA; 22310 MW;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              AAD18092.1;
203
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R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primates;
                                                                                                                                                                                                   12.3%; Score 122.5; DB 22.5%; Pred. No. 0.0021;
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                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                       S., Shaffer T.,
Loretz C., Madan
                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                   -> L.
BA0C25B7930A3A92 CRC64;
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Madan
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                                                                                                                                                                                                                                                                                                                                                                                                                                     James R.,
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                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                          Dors
                                                                                                                                                                                         78;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ratcliffe
M., Young
                                                                                                                                                                                                               Length
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                 205;
                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                       J.,
                                                                                                                                                                                        Gaps
                                                                                            134
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                                               192
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Minimum DB
Maximum DB
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Fas ligand - human
fas ligand - rat
CD40 ligand - bovi
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## ALIGNMENTS

C;Accession: A53062

R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Cell 76, 9976, 1994

A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation A;Reference number: A53062; MUID:94185175

A;Accession: A53062

A;Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>

C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

RESULT A53062

Fas ligand - mouse

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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38707; JC3240; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici A;Reference number: I38707; MUID:95127560
A;Reference number: I38707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
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I38707
Fas ligand - l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 PILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 VSSFEKQIANPSTPSEKKEPRSV-AHLTG------NPHSRSIPL-----EWEDT-Y 164
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                                                                                                                                                                                                                                      human
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                                                                                                              C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the A;Reference number: A49266; MUID:94084792
A;Accession: A49266
                                                                                                                                                                                                                                                                                                                           RESULT
A49266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 151/1; 116/3
C;Keywords: 91ycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted •
F;76,184,250,260/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731
A;Accession: I38554
                                             A; Molecule type: mRNA
A; Residues: 1-278 <SUD>
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                                                                                             A;Status:
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A; Residues: 1-281 <RE2>
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A; Residues: 1-281 <SCH>
                                                                                                                                                                                                                                                                                                        fas ligand - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Schatzlein,
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;Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Gene: FasL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRESTSQMHTASSLEKQIGHPSP-PPEKKELRKVAHLT---GKSNSRSMP------
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                                                                                                                                                              ligand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 281
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                                                                                                                                                              novel member of the
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j

cytotoxin;

glycoprotein;

lymphokine;

macrophage

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CD40 ligand - bovine
C. Species: Bos primigenius taurus (cattle)
C. Date: 08-Jul-1995 #sequence_revision 21-
C. Accession: S53090
R. Mertens, B.E.L.C.; Muriuki, M.
R. Mertens, B.E.L.C.; Muriuki, M.
   C; Superfamily:
C; Keywords: cy
                                                A;Cross-references: EMBL:X54859; NID:g2132; C;Genetics:
                                                                                A; Molecule type: DNA
A; Residues: 1-204 < KUH>
                                                                                                                 A; Reference number: S17289;
A; Accession: S17289
                                                                                                                                                                   Gene 102,
                                                                                                                                                                                                  tumor necrosis factor beta precursor - pig
c;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S17289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, Februar A;Description: Cloning of bovine CD40L and A;Reference number: S53090 A;Accession: S53090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       망
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                                  A; Introns: 32/3; 68/1
                                                                                                                                                  A; Title: The porcine tumor necrosis factor-encoding genes:
                                                                                                                                                                   R; Kuhnert, P.; Wuethrich, Gene 102, 171-178, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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A; Residues: 1-261 < MER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                     203 RILLRAANTHSSSKPC--GQQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 27.1 tes 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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                                                                                                                                                                                                                                                                                                                                                                ILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                                                                                                    TLSNNLVTLENGKQLAVKRQGFYYIYTQVTFCSNRE----TLSQAPFIASLCLKSPSGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                   FLSN--LHLRNG-ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKKKEKNFEMHKGDQEPQ-IAAHV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ-----SCNSQPLSHKVYMRNFKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISTVQEKQQNISPLVRERGPQRVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDLVLMEEKKLNYCTT--GQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP 127
Ly: tumor necrosis
cytokine; cytotoxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276
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27.5%;
                                                                                                                                                                                 C.; Peterhans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%;
                                                                                                                                MUID:91340150
                  factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 142; DB
Pred. No. 2.9e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 177.5;
Pred. No. 2.2
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                                                                                                                                                                                    E.; Pauli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ISEASSKTTSVL----QW--APKGYY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology
                                                                   PIDN:CAA38638.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                   sequence and comparative
                                                                 PID:g2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---EWEDT- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFA and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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                                                                                                                                                                                                                                                                                                                                      257
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Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF
A;Reference number: JH0309; MUID:91065534
A;Accession: JS0727
A;Accession: JS0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor alpha precursor - rabbit N;Alternate names: cachectin; TNF alpha C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: A25454; A25451; JS0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                     F;83/Binding site: c
F;147-178/Disulfide
                                                                                                                                                                                        C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymp
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Cross-references: GB: M60340; GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: this sequence differs from that shown R; Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Gene 95, 215-221, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor A;Reference number: A25451; MUID:86219712
A;Accession: A25451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Molecular cloning a A;Reference number: A25454; A;Accession: A25454
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                                                                                                                                                                                                                                                                           A; Introns: 62/3;
                                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence
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A; Residues: 1-234 <IT2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-234 <ITO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                      Query Match
Best Local S
Matches 41
                                                                                                                                                     ;19,20/Binding site: myristate (Lys) (covalent) #status ;83/Binding site: carbohydrate (Ser) (covalent) #status
                                                                                                                                                                                                                                                                                               ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157-165, 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 46; Conserv
  28 GPQRVAA----HITGTRGRSNTL-SSPNSKNEKALGRKINS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFFGAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSQYPFHVPLLSAQKSVCPGPQGPW-VRSVYQGAVFLLTQGDQLSTHTDGTPHLLLSPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLRWRANT-----DRAFLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF
                                        l Similarity
41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
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                                                                                                                                       bonds:
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                                                        13.1%; 22.9%;
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24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and expression; MUID:86219711
                                                                                                                                     #status predicted
                                                                                                                                                                                                                                                                                                               GB:M35326;
                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.; Sakamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134.5; DB 1;
Pred. No. 0.0001;
""" matches 76;
                                      Score 130.5; DB 1
Pred. No. 0.00027;
6; Mismatches 77
                                                                                                                                                                                                                                                                                                             NID:g165754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Escherichia coli of the
                                                                                                                                                                                                                                                                                                                                                                        translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:AAA31486.1; M.; Kawahara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jongeneel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         İn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  н.;
                                                                                                                                                                                                                                                                                                                                                                                                                                locus,
                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   having a Gln inserted between ngeneel, C.V.; Nedospasov, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kajihara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                              containing the
                                                                                                                                                                                                                                                                                                             PIDN: AAA31484.1;
                                                                        Length
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                                        Indels
  ----WESSRSGHSFL 74
                                                                                                                                                     predicted
predicted
                                                                                                                                                                                                                                    lymphokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:g165760
; Todd, C.W.; Wallace,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiyota, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                    macrophage;
                                                                                                                                                                                                                                                                                                             PID:g165756
                                                                                                                                                                                                                                                                                                                                                                                                                              encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues
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A; Nolecule type: DNA
A; Residues: 1-232 <KUH>
A; Residues: 1-232 <KUH>
A; Residues: 1-232 <KUH>
A; Cross-references: EMBL: X54859; NID: g2132; PIDN: CAA38639.1;
A; Note: the authors translated the codon GAG for residue 202
R; Cho1, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
submitted to the EMBL Data Library, January 1991
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                                                                                                                                                                                                                                                                              C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokin F;1-77/Domain: propeptide #status predicted cPRO> F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT> F;19,20/Binding site: myristate (Lys) (covalent) #status predicted F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted F;144-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 44-232 <PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: I46659; A; Accession: I46659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative A; Reference number: $17289; MUID: $91340150 A; Accession: $17290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X54001; NID:g2135; R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Gene 102, 171-178, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; Mc
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor necrosis factor alpha precursor pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: S12606; S17290; S18965; 146659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 62/3; 78/1; 93/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1;
R;Pauli, U.; Beutler, B.; Peterhans, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-232 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S18965
A; Accession: S18965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-232 < DRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S12606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S12606; MUID:91016861
                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                        Matches
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     85
                                                       66
                                                                                                      28
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VIHEKGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLMKSARNSCW
                                                    GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL 123
                                                                                                   GPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAIKSPCHRETPEEAEPMAWYEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGMKLTDNQLVVPADGLYLIYSQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNKVNLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDPILLM 133
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:M29079; NID:g164694; PIDN:AAA31128.1;
                                                                                                                                                                             13.1%; 25.1%;
                                                                                                                                                        30;
                                                                                                                                                     Score 130; DB 1;
Pred. No. 0.00029;
0; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA37949.1; ; Pauli, U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding porcine tumor necrosis
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                                                                                                                                                        78;
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                                                                                                                                                                                                    Length 232
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                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         lymphokine;
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es Gly
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                                                                                                                                                        20;
                                                                                                                                                     Gaps
                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                            macrophage;
                                                                                                                                                        6
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R; Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A; Title: Molecular and biological characterization of A; Reference number: S21738; MUID:92244364
A; Accession: S21738
A; Molecule type: mRNA
A; Residues: 1-260 <ARM>A; Accessions: S1738
    C;Keywords: glycoprotein; transmembrane protein F;23-46/Domain: transmembrane #status predicted <TMM>F;47-260/Domain: extracellular #status predicted <EXTF F;47-260/Domain satte: carbohydrate (Asn) (covalent) #st
                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
C;Accession: S21738
                                                                                                                                                                                                                                                                                                                                    RESULT
S21738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PITNF
A;Gene: PITNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Superfamily: timor necrosis factor
C;Reywords: glycoprotein; lipoprotein; myristylation
C;Reywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status
F;84/Binding site: carbohydrate (Ser) (covalent) #status
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                                                                                                                                                                                                                                                                                                                    CD40 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C;Accession: I54490
                                                                              A;Cross-references: EMBL:X65453; NID:g50351; PIDN:CAA46448.1;
                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-235 < R
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Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin
A;Reference number: I54490; MUID:92218012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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Best Local S
Matches 45
                                                                                                                                                                                                                                                     Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FFG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RETPEGAEAKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNLLSAIKSPC-PKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGPQREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGAN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQ 177
                                                                                                                                                                                                                                                                                                                    - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
45; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%;
24.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 129.5; DB 2; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
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predicted <EXT>
(covalent) #status predicted
                                                                                                                                                                                                                                     Sato,
                                                                                                                                                                           a murine ligand for CD40
                                                                                                                                                                                                                                   T.A.; Clifford, K.N.; Macduff, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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predicted
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                                                                            PID:g50352
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Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene A;Title: Cloning Type 201344; MUID:92084125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I46046; S24641
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lympho
A; Molecule type: .DNA
A; Residues: 1-234 <SUX>
A; Cross-references: GB:
                                                            A; Reference number: JQ1344; A; Accession: JQ1344
                                                                                                                                                                                             C;Species: Equus caballus (domestic hort) C;Date: 10-Sep-1999 #sequence_revision
                                                                                                                                                                                                               tumor necrosis factor alpha precursor N;Alternate names: cachectin; TNF alpha C;Species: Equus caballus (domestic horses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 32/
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-204 <CL2>
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                                                                                                                                                                         C; Accession: JQ1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 ---QW-AKKGYYTMKSNLVMLENGKQLTVKREGLYYVYTQVTFCSNRE----PSSQRPFI
                                                                                                                                                                                                                                                                                                                                                                                                                    180 HEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TISTVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RTSEETISTV----QEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGR 59
                                                                                                                                                                                                                                                                                                                                                                           PSSVFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPSAAQPAHQQL-PTPFTRGTLKPAAHLVGDPSTQDSLRWRANT------DRAFLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFSPQYPFHVPLLSAQKSVCPGPQGPW-VRSVYQGAVFLLTRGDQLSTHTDGISHLL-LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGLWLKPSIGSERILLKAANTHSSSQLCEQ--QSVHLGGVFELQAGASVFVNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----HGF----SLSNNSLLVPTSGLYFVYSQVVFSGRGCFPRATPTPLYLAHEVQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQFEDLVKDITLNKEEKKENSFEMQRGDEDPQIAAHV-----VSEANSNAASVL-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32/3; 68/1
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47; Conser

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                                                                                                                                                                                                                                                                                                                                                                                                                    188
  GB:M64087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 necrosis factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUID: 94083525
NID:g164244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 127.5; DB 1 Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 128.5; DB 2
Pred. No. 0.00046;
5; Mismatches 68
                                                                                                                                                                                                                      horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                               10-sep-1999
                                                                                                                                                                                                                                                               horse
  PIDN: AAA30959.1;
                                                                                                            TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                            alpha
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                                                                                                                                                                                               #text_change
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                                                                                                       encoding equine tumor necrosi
PID:g164245
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                                                                                                                                                                                               04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Genetics:
A;Ge
              A;Reference number: S26694; MUID:93076854
A;Accession: S26694
A;Status:
                                                                                                   A;Experimental source: peripheral blood T-cell R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on hu
                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-261 <SPR>
A; Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1;
                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:215017; NID:g38483; PIDN:CAA78737.1; PID:g38484 R;Spri4gs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, J. Exp. Med. 176, 1543-1550, 1992 A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and A;Reference number: JH0793; MUID:93094757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct-1999
C;Accession: I53476; S28017; JH0793; S26694; S28852; S25684; S30593
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A; Residues: 1-261 <HOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The human T cell antigen gp39, a A; Reference number: $28017; MUID:93049181 A; Accession: $28017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124 R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesc EMBO J. 11, 4313-4321, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 315, 259-266, 1992
A;Title: Human CD40-ligand: Molecular cloning,
A;Reference number: I53476; MUID:93138085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD40 ligand - human
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F;146-178/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                A; Accession: JH0793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-261 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Homo sapiens (man)
Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 VSVTNEHLIDMDHEAS-FFG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 VLLTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPWYEPIYLGGVFQLEKGDQLS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QL--QWLSGRANALLANGVKLTDNQLVVPLDGLYLIYSQVLFKGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGPQREEQLPNAFQSINPLAQTLRSSSRTPSDKPVAHVVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQ 118
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A;Title: Dense Alu clustering and a potential new member of the NFkappa A;Reference number: S36152; MUID:93272029
A;A;Accession: S36153
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C; Keywords: alvan---
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                             A; Title: Human tumour necrosis factor: precursor A; Reference number: A93351; MUID: 85086244
                                                                                                      R; Pennica, D.; Nedwin, G. Nature 312, 724-729, 1984
                                                                                                                                    A; Note: the nucleotide sequence was submitted R; Pennica, D.; Nedwin, G.E.; Hayflick, J.S.;
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-233 <IRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-233 <NED>
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A; Residues: 1-261 <GAU>
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                                                                                                                                                                                                             A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence
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not shown;

translation

not shown

NFkappaB

PID:g37210

homology and

d to the EMBL Data Library, in Seeburg, P.H.; Derynck, R.;

August 1992

Palladino, homology

structure,

expression

and

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C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; &
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.;
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homolog
                                                                                                                                                                                             tumor necrosis factor alpha precursor [validated] - N; Alternate names: cachectin; TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: glycoprotein: transmembrane protein F;13-44/Domain: transmembrane #status predicted F;45-261/Domain: extracellular #status predictec F;6,240/Binding site: carbohydrate (Asn) (covale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, CFEBS Lett. 315, 259-266, 1993
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and A;Reference number: S28852; MUID:93138085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-261 <GRA>
A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
P-Cauchat. J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:CD40LG; HIGM1; IMD3
A;Cross-references: GDB:120632; OMIM:308230
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Non-the the sequence from Fig. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 TNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSPGRFER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QW--AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCL 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 124.5; DB Pred. No. 0.0011
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C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein;
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely ut are produced by different cell types and have different induction kinetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha partitle: Myristyl acylation of the tumor necrosis factor alpha partitle: Association of myristylated lysines A;Contents: annotation; identification of myristylated lysines R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S Biol. Chem. 260, 2345-2354, 1985
J. Biol. Chem. 260, 2345-2354, 1985
J. Biol. Chem. 260, 2345-2354, 1985
J. Fittle: Human tumor necrosis factor. Production, purification, A;Reference number: A92511, MUID:85130974
A;Contents: annotation; disulfide bond
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A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Blochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A;Reference number: I53311; MUID:86030296
A;Accession: I53311
                                                                                                                                                                                                                                      A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441;
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
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Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation
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A;Cross·references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyel R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Science 228, 149-154, 1985
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A; Title: Simultaneous production of natural
A; Reference number: A61478; MUID:88301617
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A; Residues: 1-233 <MAR>
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A; Residues: 1-62, 'S', 64-233 <WAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reference number: I54522; MUID:94102809
Accession: I54522
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   /Disulfide
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OWHUA
LYMPHOTOXIN alpha precursor - human
LYMPHOTOXIN alpha precursor - human
LYMPHOTOXIN alpha precursor - human
N;Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C;Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; S36154; T54482; A93350; B32877; A91906; A61478; S26951;
C;Accession: A92755; A92755; A92755; A92755; A92756; A9275
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A, Note: the nucleotide sequence was submitted to the EMBL Data Library, A
R, Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A; Title: Haplotypic polymorphisms of the TNFB gene.
A, Reference number: I54482; MUID:91139175
A; Accession: I54482
A, Status: translation not shown; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A, Molecule type: DNA
A, Residues: I-124, P, 126-205 < RES>
A, Cross-references: GB:M55913; NID:g339742; PIDN:AAB59455.1; PID:g339743
A, Experimental source: ancestral haplotype 57.1
A, Note: 59-Asn was also found (ancestral haplotype 8.1)
                                                                                                                               A;Cross references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445 A;Experimental source: lymphoblastoid cell line RPMI-1788 R;Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986 A;Title: Tumor necrosis factors: gene structure and biological activit: A;Reference number: A32877; MUID:87217059
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A; Residues: 1-12, 'R', 14-205 <IRI>
A; Cross-references: EMBL:Z15026;
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A; Residues: 1-59,'N',61-205 <NED>
R; Iris, F.J.M.; Bougueleret, L.; Prieur,
Nature Genet. 3, 137-145, 1993
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                                                                                              A; Reference number: A; Accession: B32877
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J. Cell. Biochem. 29, 171-181, 1985
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                                                                 A; Status: preliminary; not
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A; Residues: 1-205 <GRA>
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type: m
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A;Title: Natural huma
A;Reference number: 9
A;Accession: S26951
A;Molecule type: prof
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A;Title: N-linked sugar chain structure of recombinant human A;Reference number: S34742; MUID:93311995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 56-79;86-95; X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X'
R; Voigt, C.G.; Maurer-F09y, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A; Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylat
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A;Residues: 1-59,'N',G61-205 <KOB>
A;Residues: 1-59,'N',G61-205 <KOB>
A;Cross-references: B:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A;Cross-references: Thr and ACC for R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, Lymphokine Res. 7, 175-185, 1988
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                        R;Shirai,
                                                                                                                           tumor necrosis factor alpha p: N; Alternate names: cachectin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        while having no detrimental effect on normal cells. It can also act synergistically wit:
Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differical activities but are produced by different cell types and have different induction ki
                   ;Species: Mus musculus (house mouse)
;Species: Mus musculus (house mouse)
;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000;
;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000;
;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696;
;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: GDB:LTA; LT; TNFB
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Best Local
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                                                                                                                                                                                                                                                                                      167 MYHGAAFQLTQGDQLSTHTDGIPHLV-LSPSTVFFGAF
193-201,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 92
                                                                                                                                                                                                                                                                                                                                       IYQGGIFELKENDRIFVSVTN-EHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                              FVYSQVVFSGKAYSPKATSSPLYLAHEVQLFSSQYPFHVPLL-SSQKMVYPGLQEPWLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDAEYGLYS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAHLIGDPSKQNSL
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37; Conserv
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Pred. No. 0.
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C; Keywords: Cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; F;80-235/Product: tumor necrosis factor #status experimental <maT> F;20/Binding site: myristate (Lys) (covalent) #status predicted F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-230, 'R', 232-235 <RES>
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1;
A;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylat
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J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor A;Reference number: A34251; MUID:89380231
A;Accession: A34251
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Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour
A;Reference number: A23127; MUID:85242112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-235 <SHA>
A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A;Note: article in Russian with English abstract
A;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, Nucleic Acids Res. 15, 9083-9084, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986 A;Title: Identification of a common nucleotide see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID R;Pennica, D; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA
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                                                                                                                                                           A; Note: the first intron occurs in the 5'-untranslated region
                                                                                                                                                                                      A; Introns: 62/3;
                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 80-85, 'X', 87-99
                                                                                                                                                                                                                                                                                                             A; Reference number: A36696; MUID: 91097531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 159058; MUID: 86149365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-235 < FRA>
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A; Residues: 1-235 <PEN>
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A; Residues: 1-235 <S
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A; Residues: 1-23
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                                                                                                                                   ;Superfamily: tumor necrosis factor
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